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US-10-048-197-2 x AX067463
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                                                                                                                                              ACCESSION
                                                                                                                                                                                      DEFINITION
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Ratio: 5.027
Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                  gb_ba: AE005493
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Nucleotide sequences of moraxella catarrhalis genome
Patent: WO 0078968-A 38 Z8-DEC-2000;
Incyte Genomics, Inc. (US)
Location/Qualifiers
                                                           Escherichia coli 0157:H7
Escherichia coli 0157:H7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 38
AX067463
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Bacteria; Proteobacteria; gamma subdivision;
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                     Escherichia
                                          Bacteria; Proteobacter
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gcherichia coli 0157:H7 EDL933
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/db_xref="taxon:480"
18811 c 21444 g 27367 t
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3, section 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission Submitted (22-OCT-2000) Laboratory of Genetics, University of Wisconsin, 445 Henry Wall, Madison, WI 53706, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rose,D.J., Mayhew,G.F., Evans,P.S., Gregor,J., Kirkpatrick,H.A., Posfai,G., Hackett,J., Klink,S., Boutin,A., Shao,Y., Miller,L., Grotbeck,E.J., Davis,N.W., Lim,A., Dimalanta,E., Potamousis,K., Appodaca,J., Anantharaman,T.S., Lin,J., Yen,G., Schwartz,D.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Grotbeck, E.J., Davis, N.W., Lim, A., Dimalanta, E., Potamousis, K., Apodaca, J., Anantharaman, T.S., Lin, J., Yen, G., Schwartz, D.C., Welch, R.A. and Blattner, F.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Perna, N.T., Plunkett, G. III, Burland, V., Mau, B., Glasner, J.D., Rose, D.J., Mayhew, G.F., Evans, P.S., Gregor, J., Kirkpatrick, H.A., Posfai, G., Hackett, J., Klink, S., Boutin, A., Shao, Y., Miller, L., Posfai, G., Hackett, J., Klink, S., Boutin, A., Shao, Y., Miller, L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 (bases \ Perna, N.T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genome sequence of enterohaemorrhagic Escherichia coli 0157:H7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Malch, R.A. and Blattner, F.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="0-island #108
homologous to E. coli
complement(224. .829)
/gene="23935"
                                                                            /translation="MRRTFTAEEKASVFELMKNGTGFSEIANIIGSKPGTIFTMLRDT
GGIKPHERKRAVAHLTUSEREEIRAGLSAKMSIRAIATALNRSPETIISREVQRAMGRR
YYKAVDANNRAANRAKRKPKPCLLONLPLRKLULEKLEMKMSPEDIISGENLRFTKPBC
TLRISPETIYKTLYFRSREALHHLNIOHLRRSHSLRHGRRHTRKGERGTINIVNGTPA
                                                                                                                                                                                                                                                                             /note="Residues 1 to 247 of 251 are 100.00 pet
to residues 1 to 247 of 383 from GenPept 118
gi|7800288|gb|AAF69884.1|AF250878_45 (AF250878)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="makfrkplrrkkamakparårcnrkredlxykrifellsfdkst
Gyfrwkyptqgrialnsvagafdsngysmimidgarykthylyfyithnrwpagqidh
yngirtdnrpenlreclpiensrnirirknsksgcqgytwhkrqkkwnyklgfhgksk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Residues 82 to 187 of 201 are 30.84 pct identical to residues 13 to 118 of 121 from GenPept 118 : gi 15583|emb|CAA24404.1| (VDM146) gene 3.8 [Bacteriophage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(224. .829)
/gene="Z3935"
                                                                                                                                                      /transl_table=11
/product="IS30 transposase"
/protein_id="AAG57749.1"
/db_xref="GI:12517069"
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/strain="EDL933
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                                                                                                                                                                                                                                                            transposase [Salmonella typhi]"
                                                                                                                                                                                                                                                                                                                                            Sequence Associated)
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                                                                                                                                                                                                                                       'codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="tra8_3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="unknown protein encoded /protein_id="AAG57748.1"
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                                                         ERSRNIDNRRSLGHWEGDLVSGTKNSHIDSFF*
                                                                                                                                                                                                                                                                                                                                                                                   'gene-"tra8_3"
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sociated)"
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9b_hr:AL137850

9b_ht:AC011161

9b_ov:AF173857

9b_pr:AL512598

9b_ht:AF001795

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9b_ht:AC099643

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gb_htg:AC101573
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                                          gb_htg:AC067965
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gb_htg:AC009452
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gb_htg:AC099358
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gb_htg:AL356370
gb_htg:AL138848
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Database length: 1873333701
Search time (sec): 1887.650000
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Ouery: US-10-048-197-2
Ouery length: 111
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gb_ba:AF421351
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gb_ba:AE005493
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-(0-/cgn2_1/USPTO_spool/US10048197/runat_17092002_135849_22601/app_query.fasta_1.168
-DB=Genemb1 -QFWT=fastap -SUFFIX-std.rge -GAPOP-12.000
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                                                                                                   984 i AC042438 Rattus norvegicus of 322 i AL627214 Mus musculus chromod 1 AF19465 Neisseria meningitidis 1 A68918 Sequence 99 from Patent 1 AX024066 Sequence 99 from Patent 1 AX024066 Sequence 9 from Patent 1 AX024066 Sequence 1 from patent 1 AX023695 Sequence 1 from patent 1 AX023695 Sequence 1 from patent 1 AX023695 Sequence 1 from patent 1 AX023697 Sequence 1 From patent 1 AX023697 Polynucleotide of Str 1 AE007477 Streptococcus pneumo 1 AE007477 Streptococcus pneumo 1 AX021268 Homo sapiens chromod 1 AL162430 Human DNA sequence 1 AL137897 Xenopus laevis recept 1 AL137897 Xenopus laevis recept 1 AF173857 Xenopus laevis recept 1 AF173857 Xenopus laevis cept 1 AF173857 Xenopus laevis cept 1 AF03245 Human DNA sequence 1 AF03363 Human DNA sequence 
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1 AX067463 Sequence 38 from Pat
1 AE005493 Escherichia coli 015
5 1 AP002562 Escherichia coli 01
1 AC101573 Mus musculus clone F
ALI449924 Streptococcus pneum
AC009452 Homo sapiens chrome
AC099358 Rattus norvegicus c
ALI37020 Human DNA sequence
AC099386 Rattus norvegicus c
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gb_ba:AP003589
gb_pl:ATT4D2
gb_htg:AC106635
gb_htg:AP003572
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ORIGIN
    seq_documentation_block:
LOCUS AX067463
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alignment_block:
US-10-048-197-2 x AX081233
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Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
                                                                                                                                        67 lValIIeLysPheGlyHisThrAlaIIeLeualaProAsnArgTrpGlnG
                                                                                                                                                                                                                                                                                                                                   LysAsnLeuSerPheTyrLeuThrAlaLysAla 111
                                                                                                                                                                             GluIleSerSerArgPheGlySerAlaAspSerIleSerPheMetIleVa
                                                                                                                                                                                                                                GGTAATAAAATTTGGACATACCGCCATACTCGCTCCAAACCGATGGCAAG
                         AAGAACTTGTCATTTTATTTGACAGCAAAGGCA
gb_pat:AX067463
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Sequence 1 from Patent WO0109337.
AXOB1233
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1 (bases 1 to 336) .
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/db_xref="taxon:480"
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Gaps: 0
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341880 | AP003589 Nostoc sp. PCC 7
92611 | AL132958 Arabidopsis thali
135538 | AC106635 Rattus norvegicu
169761 | AP003572 Oryza sativa chr
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94750

DNA

PAT 24-JAN-2001

from Patent WO0078968.

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KEYWORDS
SOURCE '
ORGANISM
                                   REFERENCE
                                                                                                                                                                                                                    Seq_documentation_block: LOCUS AE005493
                                                                                                                                                 VERSION
                                                                                                                                                                   ACCESSION
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SOURCE
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Ratio: 5.027
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                                   Bacteria; Pr
Escherichia.
1 (bases 1
                                                           Escherichia coli 0157:H7 |
Escherichia coli 0157:H7 |
Bacteria; Proteobacteria;
                                                                                                                                        AE005493 AE005174
AE005493.1 GI:12
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Patent: WO 0078968-A 38 28-DEC-2000;
Incyte Genomics, Inc. (US)
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Moraxella catarrhalis
Bacteria; Proteobacteria;
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                             1 to 10701)
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/db_xref="taxon:480"
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                                                       gamma subdivision;
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                                                   Enterobacteriaceae;
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Submitted (22-0CT-2000) Laboratory of G
Wisconsin, 445 Henry Mall, Madison, WI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Perna, N.T., Plunkett, G. III, Burland, V., Mau, B., Glasner, J.D., Rose, D.J., Mayhew, G.F., Evans, P.S., Gregor, J., Kirkpatrick, H.A., Posfai, G., Hackett, J.F., Klink, S., Boutin, A., Shao, Y., Miller, L., Grotbeck, E.J., Davis, N.W., Lim, A., Dimalanta, E., Potamousis, K., Apodaca, J., Anantharaman, T.S., Lin, J., Yen, G., Schwartz, D.C., Welch, R.A., and Blattner, F.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Perna, N.T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Perna, N.T., Plunkett, G. III, Burland, V., Mau, B., Glasner, J.D., Rose, D.J., Mayhaw, G.F., Evans, P.S., Gregor, J., Kirkpatrick, H.A., Posfai, G., Hackett, J., Klink, S., Boutin, A., Shao, Y., Miller, L., Grotbeck, E.J., Davis, N.W., Lim, A., Dimalanta, E., Potamousis, K., Apodaca, J., Anantharaman, T.S., Lin, J., Yen, G., Schwartz, D.C., Welch, R.A. and Blattner, F.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genome sequence of enterohaemorrhagic Escherichia coli 0157:H7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (bases 1 to 10701)
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1941. 2219
                                                                                                                                                                                                                                      /function="putative enzyme; Transposases (Insertion Sequence Associated)" [251 are 100.00 pct identical foresidues 1 to 247 of 383 from GenPept 118; gi|7800288|gb|AAF69884.1|AR250878_45 (AF250878) IS30
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1126, 1881
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1126. 1881
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1941. .2210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="enterohemorrhagic"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1. .10701
                                                                                                                                                                                                                                  [Salmonella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Region of the K-12 MG1655"
                                                                                                                                                                                                                                typhi]"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              f Genetics, Un
WI 53706, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EDL933 chromosome not
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P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               [Bacteriophage
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
                                                                                              2025
                                                                                                                                                                                          1978
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                                                                                                                                        67
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gene

CDS

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alignment_block:
us-10-048-197-2 x AE005493
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||| ::::::|||||| || ||| ::::::|||:::::
1878 CTGACCTTGGCAGGTTGTTCTTCAGTAGCAACCAGTCATTGAAAAATGA 1927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2075 AACCTCTTTCATCCCCGTTGTGGGACTGCTTGCAGGTGGCGCAGACTCAC 2124
                                                                                                                                                                                                                                                                                                                                                                                                                                                            .ValValIleLysPheGlyHisThrAlaIleLeuAlaProAsnArgTrpG
:::||| ::: |||||||||
                                                                                         lnGluIleLeuSerLeuIleIleSerPheLeuTrpValLysProTyrArg
                                                                                                                                                                                                   GATGGTGAAGAACAATGGTCATACACTATGTATAACAGCCAGTCCAAAGC
                                                                                                                                                                                                                                                                                                                                                                                                       AGGACGTGTTAGCATCGTTCGGTGAACCTGACAGCCGTTCT...TTGATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(6455. .7780)
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complement(6455. .7780)
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VNEHRIKDIPVVDLNEFGLT"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121.50
1.960
66.667
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IFMNLDKITETKRIEDFLYDLTTDFFHMKNSVMSKLLKHFPSKFDVRSERTNSYIELN
ARRFRYTLGSRLANEGASIEVIAKALDHKSVNSSIIYIKNNPDNVYDIDKRLSAFFNP
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(Phage or Prophage Related)"
/note="No significant matches"
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Gaps: 2
Identity: 34.409
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seq_documentation_block:
                                                                                                                                                                                                                                                                    Hayashi,T.

Direct Submission
Submitted (26-JUN-2000) Ken Kurokawa, Osaka University, Genome Information Research Center; 3-1, Yamadaoka, Suita, Osaka 565-0871, Japan (E-mail:ken@gen-info.osaka-u.ac.jp, URL:http://www.gen-info.osaka-u.ac.jp/, Tel:81-6-6879-8365, Fax:81-6-6879-2047)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ohnishi, M., Kurokawa, K., Makino, K., Yasunaga, T., Shinagawa, H. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and genomic comparison with a laboratory strain K-12 DNA Res. 8 (1), 11-22 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hayashi,T., Makino,K., Ohnishi,M., Kurokawa,K., Ishii,K., Yokoyama,K., Han,C.-G., Ohtsubo,E., Nakayama,K., Murata,T., Tanaka,M., Tobe,T., Iida,T., Takami,H., Honda,T., Sasakawa,C., Ogasawara,N., Yasunaga,T., Kuhara,S., Shiba,T., Hattori,M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAACTAAATCTCTGACAGTTTCTTTCA 2151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ProLysAsnLeuSerPheTyrLeuThr 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Complete nucleotide sequence of the prophage VTI-Sakai carrying the Shiga toxin 1 genes of the enterohemorrhagic Escherichia coli 0157:H7 strain derived from the Sakai outbreak Gene 258 (1-2), 127-139 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Yokoyama,K., Makino,K., Kubota,Y., Watanabe,M., Kimura,S.,
Yutsudo,C.H., Kurokawa,K., Ishii,K., Hattori,M., Abe,H., Iida,T.,
Yamamoto,K., Hayashi,T., Yasunaga,T., Honda,T., Sasakawa,C. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9b_ba:AP002562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Comparative analysis of the whole set of rRNA operons between an enterohemorrhagic Escherichia coli O157:H7 Sakai strain and an Escherichia coli K-12 strain MG1655
Syst. Appl. Microbiol. 23 (3), 315-324 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ohnishi,M., Murata,T., Nakayama,K., Kuhara,S., Hattori,M.,
Kurokawa,K., Yasunaga,T., Yokoyama,K., Makino,K., Shinagawa,H. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Complete nucleotide sequence of the prophage VT2-Sakai carrying the verotoxin 2 genes of the enterohemorrhagic Escherichia coli O157:H7 derived from the Sakai outbreak Genes Genet. Syst. 74 (5), 227-239 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Makino,K., Yokoyama,K., Kubota,Y., Yutsudo,C.H., Kimura,S., Kurokawa,K., Ishii,K., Hattori,M., Tatsuno,I., Abe,H., Iida Yamamoto,K., Ohnishi,M., Hayashi,T., Yasunaga,T., Honda,T., Sasakawa,C. and Shinagawa,H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; gamma subdivision;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Escherichia coli 0157:H7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Escherichia coli 0157:H7 (strain:0157:H7,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (bases 1 to 270365)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AP002562.1 GI:13362858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Escharichia coli O157:H7 DNA, complete genome, section
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (sites)
                                                                                                        /organism="Escherichia coli/strain="0157:H7"
/sub_strain="RIMD_0509952"
                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                      0157:H7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sub_strain:RIMD 0509952)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Enterobacteriaceae;
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be,H., Iida,T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BCT 07-MAR-2001
on 13/20.
                                                                                                                                                                                                      gene
                                                                                                                                         SCDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CDS
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                                                                           complement(3364. .5214)
/gene="ECs3392"
                                                                                                                                                                                                              /Protein_id="BAB36814 1"
/db_xref="GT:13362862"
/translation="MPKIVILPHODLCPDGAVLEANSGETILDAALRNGIEIEHACEK
SCACTTCHCIVREGFDSLPESSEQEDDMLDKAWGLEPESRLSCQARVTDEDLVVEIPR
                                                                                                                                                       /gene="ECs3392"
/note="similar to HSCA_ECOLI gi|1788875
100 in 616 aa (Conserved in E.coli K-12)
                                                                                                                                                                                                                                                                                                                                                                                /evidence=not_experimental
/product="[2FE-2S] ferredo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="similar to FER_ECOLI gi|119999|sp|P25528 percent identity 100 in 111 aa (Conserved in E.coli K-12)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(3027. .3362)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(3027. .3362)
/gene="ECs3391"
                                                                                                                                                                                                                                                                                                                                                                                                                                                     /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="MGLKWTDSREIGEALYDAYPDLDPKTVRFTDMHQWICDLEDFDD
DPQASNEKILEAILLVWLDEAE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="ECs3391"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="hypothetical protein"
/protein_id="BAB36813.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="identical to YFHJ_ECOLI g1|1788873 (Conserved E.coli K-12)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product "putative peptidase"
/franslation "mppscunantiaekswgcolaallorritkmtenkritstopad
/rtanslation "mppscunantiaekswgcolaarkritstopad
/rtanslation "mppsc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /evidence=not_experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(2815. .3015)
/gene="ECs3390"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="ECs3390"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NTGSAAYPAGASTAAGFLSHFVENYQQGWLHIDCSATYRKAPVEQWSAGATGLGVRTI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="similar to PEPB_ECOLI gi|1788872 percent identity
99 in 456 aa (Conserved in E.coli K-12)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /evidence=not_experimental
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/gene="ECs3389"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="enhanced serine
/protein_id="BAB36811.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98 in 261 aa (Conserved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /evidence=not_experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(435. .1220)
/gene="ECs3388"
complement(435. .1220)
/gene="ECs3388"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'note="similar to SSEB_ECOLI gi|1788871 percent identity
98 in 261 aa (Conserved in E.coli K-12)"
                                                                                                                                                                         .5214)
                                                                                                                                                                                                                                                                                                                                                                         ferredoxin"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sensitivity"
                  percent identity
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FEATURES COMMENT

source

JOURNAL MEDLINE REFERENCE

TITLE

AUTHORS

TITLE JOURNAL

REFERENCE AUTHORS

MEDLINE

JOURNAL

TITLE

JOURNAL MEDLINE REFERENCE

TITLE

AUTHORS

JOURNAL MEDLINE REFERENCE

AUTHORS

TITLE

KEYWORDS SOURCE

ORGANISM

VERSION ACCESSION

DEFINITION

seq_name:

REFERENCE

AUTHORS

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alignment_block:
US-10-048-197-2 x AP002562
                                                                                                                                                                                                                               alignment_scores
                                                                                                                                              Ratio:
Percent Similarity:
Align seg 1/1
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   AP002562
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DDAQRQTKDAARLAGLHVLRLLNEPTAAAIAYGLDSGQEGVIAVYDLGGGTEDISIL
RLSRGVFEVLATGGDSALGGDEDHLLADY IREQAGIFDRSDNRVQRELLDAAIAAK I
ALSDADSYTVNVAGWGEBISRRQFNELIAPLVRRTLLACRRALKDAGVREDEVLEVVM
VGGSTRVPLVRERVGEEFGRPPLTSIDPDKVVAIGAAIQADILVGNKPDSEMLLLDVI
PLSTGLEVEN IPRNTTIPVARAQDFTTFKDGQTAMSIHVMGGSRELVQDCRS
LARFALRGIPALPAGGAIIRYTFQVDADGLLSVTANEKSTGVEASIQVREYSGUTDSA
LARFALRGIPALPAGGAIIRYTFQVDADGLLSVTANEKSTGVEASIQVREYSGUTDSE
IASMIKDSMSYAEQDVKARMLAEQKVEAARVLESLHGALAADAALLSAAERQVIDDAA
ALLSEVAQGDDVDAIEQAIKNVDKQTQDFAARRNDQSVRRALKGHSVDEV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="MSITLSDSAAARVNTFLANRGKGFGLRLGVRTSGCSGMAYVLEFVDEPTPEDIVFEDKGVKVVVDGKSLQFLDGTQLDFVKEGLNEGFKFTNPMVKDECGCGESFHV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(8842..6165)
/gene="ECs3394"
complement(8842..6165)
/gene="ECs3394"
/note="similar to ISCA_ECOLI g1|1788877 percent identity
100 in 107 aa (Conserved in E.coli K-12)"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="molecular chaperone"
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DEIEQAKDEARLESFIKRVKKMFDTRHQLMVEQLDNETWDAAADTVRKLRFLDKLRSS
AEQLEEKLLDF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(5231. .5746)
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complement(5231. .5746)
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/note="similar to HSCB_ECOLI gi|1788876 percent identity
100 in 171 aa (Conserved in E.coli K-12)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /evidence=not_experimental
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ADHEGRHLLPSVVHYQQQGHSVGYDARTNAALDTANTISSVKRLMGRSLADIQQRYPH
                                                                                                                                           121.50
1.960
66.667
                                                                                                                                                                                                                                                                                                /translation="MAYSEKVIDHYENPRNVGSFDNNDENVGSGMVGAPACGDVMKLQ
IKVNDEGIIEDARFKTYGCGSAIASSSLVTEWVKGKSLDEAQAIKNTDIAEELELPPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(6182. .6568)
/gene="ECs3395"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(6182. .6568)
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identity 100 in 128 aa (Conserved in E.coli K-12)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /codon_start=]
   from:
                                                                                                                                           Length:
Gaps:
Percent Identity:
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6
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REFERENCE
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AUTHORS
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ORGANISM
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KEYWORDS
                                                                                                                                                                                   COMMENT
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LOCUS AC101573
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                                                                                                                                                                                                                                                                                RS Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Boguslavkiy, L., Boukhgalter, B., Anderson, S., Camarata, J., Campoplano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ginde, S., Godd, S., Goyette, M., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Godd, S., Goyette, M., Graham, L., Grand Pierre, N., Hagos, B., Heaford, A., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Liu, G., MacLean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., McPheeters, R., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Muyen, C., Norman, C. H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Taviss, N., Travis, N., Trigillo, J., Vassillev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G., Zalnoun, J., Zembek, L., Zimmer, A. and Zody, M.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                        Submitted (23-NOV-2001) Whitehead Institute/MIT Center Research, 320 Charles Street, Cambridge, MA 02141, USA All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mammalia; Eutheria; Rodentia; Sci
1 (bases 1 to 7398)
Birren,B., Linton,L., Nusbaum,C.
Mus musculus, clone RP23-197A22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AC101573 73989 bp Mus musculus clone RP23-197A22,
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HTG; HTGS_PHASE0.
                                                                                                            http://ftp.genome.washington.edu/RM/RepeatMasker.html
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                                                                                                                                                                                                                                                                      Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (bases 1 to 73989)
Center: Whitehead Institute/ MIT Center for Genome Research Center code: WIBR Web site: http://www-seq.wi.mit.edu
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LOW-PASS SEQUENCE SAMPLING
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overlap relationships among clones to be deduced.
However, it should not be assumed that this clone will be sequenced to completion. In the event that the record is updated, the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NOTE: This record contains 92 individual
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9706 10396: contig of 10397 10496: gap of 10396
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8787 8886: 9ar
9605: 1
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Center clone name: 197_A_22
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                                                                                                              5 19394: gap of 10
5 20106: contig of 7
7 20206: gap of 10
7 20911: contig of 7
                                                                                                                                                                              1 17695: contig of
6 17795: gap of
1 18482: contig of
3 18582: gap of
1 19294: contig of
5 19304: contig of
                                                                                                                                                                                                                                                                                             3 16172:
                       22616: gap of
23310: cor
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7 7983: contig of 100
14 8083: gap of 100
14 8786: contig of
                                                                                                        21011:
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7166: /
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6 4845; gap
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0 1536: cr
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                                                                                                                                                                                                                                                                                                                                                                                                                                     1496; gap of 100 bp 1
11200: contig of 704 bp 1
11300: gap of 100 bp
12012: contig of 712 bp
12012: are of 100 bp
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3934: co
                                                                                21711: cc.
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                                                       22516: con
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13614: contig of 699 bp in
114: gap of 100 bp
1428: contig of 714 bp in
                                                                                                                                                                                                                                                 17695
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12815: contig of 703
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                                                                                   contig of 700
                                                                                                                                                                                                                                                                         contig of 718 bp
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contig of 701 bp in
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                                                                                                                                                                                                                                      100 bp
of 705 bp in
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of 702 bp in
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29755: contig of
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23411. 24116: contig
24117 24216: gap of
                                                                                                                                  100 bp

4/360: contig of 672 bp 1

61 47460: gap of 100 bp

51 48180: contig of 720 bp 1.

1 48280: gap of 100 bn

1 48967: conti
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5 45084; gan
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11 42670: gap of 100 bp
11 43368: contig of 698 b
19 43468: gap of 100 bp
19 44188: contig of 720 b
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                                             51408: cc
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                                                                                                                                                                                                                                                                                                                                                                                                   25834:
                                                                         100 bp
49770: contig of 703 bp
370: gap of 100 bp
50580: contig of 710 bp
                    08: gap of 52241: cont
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 910: gap of 10
38582: contig of (682: gap of 10
39384: contig of
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: gap of
40168: C
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31372: contig of 1
(1472: gap of 1
32164: contig of (
2264: gap of 1
32940: contig of (
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37810: contig of 706
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98: gap of
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37004: contig of 706 bp
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27355: contig of 707 b
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                                             p of 100 bp
contig of 728 bp in
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of 702 bp in
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Rattus.

(CE 1 (bases 1 to 140984)

(CE 1 (bases 1) to 140984)

(CE 2 (bases 1) to 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       47 rAsnLysGlnGluIleSerSerArgPheGlySerAlaAspSerIleSerP 64
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Ratio: 1.598
Similarity: 66.234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                oTyrArgProLysAsnLeuSerPheTyrLeu 107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rattus norvegicus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HTG; HTGS_PHASE1.
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53051 53180: gap of 715 bp in length

53166 53965: gap of 100 bp

53966 54654: contig of 689 bp in length

54655 54754: gap of 100 bp

54755 5566: gap of 712 bp in length

54675 5566: gap of 100 bp
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IN PROGRESS ***,
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Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L., Lil, J., Lil, Z., Lichtarge, O., Lien, C., Liu, J., Liu, W., Loulsege, M., Loucler, R., Lind, R., Koulsege, M., Loucler, R., Lind, R., Man, J., Mahshwari, M., Mapua, P., Martin, R., Martinde, A., Martinez, E., Massey, E., Marhiney, E., Kleed, M., P., Meador, M., Martinez, E., Massey, E., Marhiney, E., Kleed, M., P., Meador, M., Martinez, E., Massey, E., Marhiney, E., Kleed, M., P., Meador, M., Martinez, E., Massey, E., Marhiney, E., Kleed, M., P., Meador, M., Mayuyen, A., Nguyen, M., Nguyen, N., Nickerson, E., Mochaka, F., Pull, L., Oulles, M., Morris, S., Moser, M., Nickerson, E., Mochaka, F., Pull, J., Newtson, M., Nguyen, M., Nguyen, N., Nickerson, E., Mochaka, T., Shen, H., Shooshtari, N., Stone, H., Sutton, A., Svatek, A., Tabor, P., Telfford, B., Thomas, N., Nisson, H., Sutton, A., Svatek, A., Tabor, P., Telfford, B., Thomas, N., Tandris, M., Tabor, P., Telfford, B., Thomas, N., Tandris, M., Tandris, M., Tandris, M., Tandris, M., Tabor, P., Telfford, B., Thomas, N., Tandris, M., ```

JOURNAL REFERENCE

TITLE

AUTHORS TITLE

JOURNAL

COMMENT

NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/Genbank\_draft\_data.html).

NOTE: This is a 'working draft' sequence. It currently

consists of 61 contigs. The true order of the pieces

is not known and their order in this sequence record is

arbitrary. Gaps between the contigs are represented as

runs of N, but the exact sizes of the gaps are unknown.

This record will be updated with the finished sequence

as soon as it is available and the accession number will

be preserved. 21536 23975 24075 28395 28495 33267 3814 3914 8565 8665 12410 12510 16845 16945 3813: contig of 3813 bp in length 3913: gap of unknown length 8564: contig of 4651 bp in length 8664: gap of unknown length 12409: contig of 3745 bp in length 12509: gap of unknown length 16844: contig of 4335 bp in length gap of unknown contig of 4772 gap of unknown gap of contig gap of unknown contig of 2439 gap of unknown contig of 4320 of 4491 unknown bp in bp in bp in length bp in length length length length length length length

length

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14 76043 gap of unkn
14 78936 contig of 2
15 79936 contig of 2
17 79936 contig of 2
18 80901 contig of 1
18 81001 gap of unkn
18 8188 contig of 2
18 8288 gap of unknow
18 9770 contig of 10
18 9976 contig of 19
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19 908 gap of unknown
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VERSION
KEYWORDS
 DEFINITION
 seq_documentation_block:
LOCUS AL627314
 seq_name: gb_htg:AL627314
 alignment_block:
US-10-048-197-2
 alignment_scores:
 Quality:
 ORGANISM
 Align seg 1/1 to: AC094388 from: 1
 Percent Similarity:
 47612 ATGCCCGACTATCGATGTGCATAATGGTTGTGATTCGCGTTTTCCTTTAT 47661
 47562 ACAAGCCACATTATTGGGAGAAATTGTGAGCAGGTTTGGGGGAATGGTTAT 47611
 47512
 47462 TTGTTGAATTTCAGGCCAGTGAGAGACCCATTGTCAAAGGGGGAAGAAC 47511
 5 HislleArgLeuThrIleSerAlaLeuLeuThrAlaLeuLeuValThrGl
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47362 CACATATTGACAAAGAAGTCCGTCATGCTGCGCATTGCTTATAGTGCCAGG
 47412
 74 ThralaileLeuAla 78
 58
 49 LysGln.....
 34AsnGlnGlnThrIleGluGlnThrIleIleLysGlyLysThrAsn 48
 51
 21 y.......CysValSerThrGlyAsnValAlaMetLysGluGln.... 33
 GluIleSerSerArgPheGly......
 ACAGCAATGTTTGCC 47676
 ..SerAlaAspSerIleSerPheMetIleValValIleLysPheGlyHis
 TCCCAAGAACACGTGTGGGGCCTCCATCTTCCGCACACAGATGCATTA 47561
 GCATGGCAGGTGTCGATCCTCTGGCTTTCTCTCGCTCCGGCATAGACTAT 47461
 Mus musculus chromosome 4 clone RP23-354H24, *** SEQUENCING IN AL627314.5 GI:18152585
HTG; HTGS_PHASE2; HTGS_ACTIVEFIN; HTGS_DRAFT; HTGS_FULLTOP. house mouse.

Mus musculus
 Ratio:
 126214
126314
128132
128232
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129945
131545
131645
133141
133241
133241
 x AC094388
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1116434
1117930
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1121419
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123314
 124794
 124694
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1.509
51.429
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Gaps:
Percent Identity:
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106536 107745 107845 109564 109664 112051 112151 113413 113513

100655 100755 101949 102049 103516 103516 103616 105212

94848 94948 96552 96652 98299

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50

87871 88939 89039 91037 91137 93365 93465

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 Center project name: bM354H24
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 Contact: humquery@sanger.ac.uk
Project Information
 Brown, A.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus
 Center code: SC
 Center: Wellcome Trust Sanger Institute
 Direct Submission
 NOTE: This is a 'working draft' sequence.
This sequence will be replaced
by the finished sequence as soon as it is available and
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* as soon as it is available and the accession number will
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 Direct Submission
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 A68918
 2 (bases 1 to 267)

Perrin,A., Nassif,X. and Tinsley,C.R.

Direct Submission

Submitted (16-JUL-1999) Necker Medicine Faculty,

rue de Vaugirard, Paris 75015, France

Locatron/Qualifiers
 1 (bases 1 to 267)
Perrin,A., Nassif,X. and Tinsley,C.R.
Identification of regions of the chromosome of Neisseria meningitidis and Neisseria gonorrhoeae which are specific
 Neisseria meningitidis.
Neisseria meningitidis
Bacteria; Proteobacteria; beta subdivision; Neisseriaceae;
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Nassif,X., Tinsley,C., Aujame,L., P
Bouchardon,A. and Renauld,M.G.
Patent: FR 2785293-A 9 05-MAY-2000;
PASTEUR MERIEUX SERUMS VACC (FR)
 Patent: WO 9802547-A 89 22-JAN-1998;
INST NAT SANTE RECH MED (FR)
Other publication FR 2751000 19980116
 Nassif,X., Tinsley,C., Achtman,M., Ruelle,J., Vinals,C. and Merker,P.

Merker,P.

DNA AND SPECIFIC PROTEINS OR PEPTIDES OF THE NEISSERIA MENINGITIDIS SPECIES BACTERIA, METHOD FOR OBTAINING THEM AND THEIR BIOLOGICAL
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Neisseria meningitidis
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 Current sequence finishing criteria for the C. elegans genome sequencing consortium are that all bases are either sequenced unambiguously on both strands, or on a single strand with both a dye primer and dye terminator reaction, from distinct subclones. Exceptions are indicated by an explicit note.

EXCEPTIONS are indicated by an explicit note.

It may be shorter because we only sequence overlapping sections
 Submitted (23-JUN-1995) Nematode Sequencing Project, Sanger Institute, Hinxton, Cambridge CB10 1SA, England and Department of Genetics, Washington University, St. Louis, MO 63110, USA, E-mail: jes@sanger.ac.uk or rw@nematode.wustl.edu COding sequences below are predicted from computer analysis, using predictions from Genefinder (P. Green, U. Washington), and other
 neighbouring
 Sulston, J.E.
 The C.elegans Sequencing Consortium 2 (bases 1 to 38240)
 Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium Science 282 (5396), 2012-2018 (1998)
 Direct Submission
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 Eukaryota; Metazoa; Nematoda; Rhabditoidea; Rhabditidae; Pe
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 Z49907.1 GI:872034
 Caenorhabditis elegans
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 or longer because we arrange for a small overlap between
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 IMPORTANT: This sequence is NOT necessarily the entire insert of the specified clone. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between neighbouring submissions.
 sequence Z48367.

For a graphical representation of this sequence and its analysis see: http://wormbase.sanger.ac.uk/perl/ace/elegans/seq/sequence?
 sequence Z48367.

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COMMA EST YKJUDUS COMES FROM this gene; CDNA EST YK11491.5 comes from this gene; CDNA EST YK11491.5 comes from this gene; CDNA EST YK187e10.3 comes from this gene; CDNA EST YK187e10.5 comes from this gene; CDNA EST YK197e6.5 comes from this gene; CDNA EST YK375c6.5 comes from this gene; CDNA EST YK375c6.5 comes from this gene; CDNA EST YK371c6.5 comes from this gene; CDNA EST YK381h7.3 comes from this gene; CDNA EST YK280b1.3 comes from this gene; CDNA EST YK280b1.3 comes from this gene; CDNA EST YK292g4.3 comes from this gene; CDNA EST YK292g4.3 comes from this gene; CDNA EST YK262e9.3 comes from this gene; CDNA EST YK262e9.5 comes from this gene; CDNA EST YK262e3.3 comes from this gene; CDNA EST YK222e2.3 comes from this gene; CDNA EST YK222e2.3 comes from this gene; CDNA EST YK228g9.5 comes from this gene; CDNA EST YK238f5.5 comes from thi
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CDS

gene

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Klee,S.R., Morelli,G., Basham,D., Brown,D., Chillingworth,T.,
Davies,R.M., Davis,P., Devlin,K., Feltwell,T., Hamlin,N.,
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 Neisseria meningitidis serogroup A strain
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AL162753 AL157959
AL162753.2 GI:7379120
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Neisseria meningitidis 22491
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 Submitted (30-MAR-2000) Submitted on behalf of the Neisseria sequencing team, Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 ISA E-mail: parkhill@sanger.ac.uk
 veicalis of N. meningitidis sequencing at the Sanger Centre are available on the World Wide Web.
 Quail, M.A., Rajandream, M.A., Rutherford, K.M., Simmonds, M., Skelton, J., Whitehead, S., Spratt, B.G. and Barrell, B.G. Complete DNA sequence of a serogroup A strain of Neisseria meningitidis 22491
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 (URL,
 Direct Submission
 Parkhill, J
 Nature 404 (6777), 502-506 (2000) 20222556 2 (bases 1 to 349061)
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 CCAATGCTATGTTACCAGTGTAATCAGCACAATCGGCGTTACCACTTCCG 149409
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57

6

90

CDS

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 65312 bp DNA linear HTG 23-NOV-2001 Mus musculus clone RP24-346C14, LOW-PASS SEQUENCE SAMPLING. AC102510 AC102510.1 GI:17061596 HTG; HTGS PHACEO
 Submitted (23-NOV-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA I repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
 Birren,B., Linton,L., Nusbaum,C. and Lander,E. mus musculus, clone RP24-346C14
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
1 (bases 1 to 65312)
 Mus musculus
 Unpublished
 NOTE: This record contains 83 individual sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced. However, it should not be assumed that this clone.
 will be sequenced to completion. In the event that
 the record is updated, the accession number will
 Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L18939
Center clone name: 346_C_14
 Center: Whitehead Institute/ MIT Center for Genome Research Center code: WIBR
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662 761: gap of 100 bp
762 1435: contig of 6674 bp in length
1436 1535: gap of 100 bp
1536 2216: contig of 681 bp in length
1535: gap of 100 bp 1216: contig of 681 bp in length 2316: gap of 100 bp 3017: contig of 701 bp in length
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3117: gap 3807:

contig

100 bp

4676: 3907:

4576: con 5353:

gap of

bp in length bp in length

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100 bp of 686 bp in

length

100 bp of 694 bp in length

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33925 34613: con
 33013 33112:
 31499 32195: contig of 697 bp
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of 712 bp in
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F 30-OCT-1997 JP 1998520718

R 31-OCT-1996 US 60/029960

I CHARLES A KUNSCH,GIL H CHOI,PATRICK J DILLON,CRAIG A ROSEN, PI
STEVEN C BARASH,
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Direct Submission
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Location/Qualifiers
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Genome of the Bacterium Streptococcus pneumoniae Strain
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 Peterson, S., Heidelberg, J., DeBoy, R.T., Haft, D.H., Dodson, R.J., Durkin, A.S., Gwinn, M., Kolonay, J.F., Nelson, W.C., Peterson, J.D., Umayam, L.A., White, O., Salzberg, S.L., Lewis, M.R., Hansen, C.L., Holtzapple, E., Khouri, H., Wolf, A.M., Utterback, T.R., Hansen, C.L., McDonald, L.A., Feldblyum, T.Y., Angiuoli, S., Dickinson, T., Hickey, E.K., Holt, I.E., Loftus, B.J., Yang, F., Smith, H.O.,
 Complete genome sequence of a virulent isolate of Streptococcus
 Venter, J.C., Dougherty, B.A., Morrison, D.A., Hollingshead, S.K. and
 Science. 293 (5529), 498-506 (2001)
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Waterston, R. H.
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University School of Medicine, 44
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 2 (bases 1 to 166516)
Andrews,S., Stoneking,T. and Gibson,A.
The sequence of Homo sapiens BAC clone RP11-196J6
 NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap
 Direct Submission
Submitted (19-OCT-1999) Genome
University School of Medicine,
MO 63108, USA
 Unpublished
3 (bases 1
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Sulston, J. E. and Waterston, R.
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 Waterston, R.
between neighboring data submissions.
 Toward a complete human genome sequence Genome Res. 8 (11), 1097-1108 (1998)
 Homo sapiens
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 Center project name: H_NH0196J06
 Web site: http://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu
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 GI:10047984
 Summary Statistics
 166516 bp
RP11-196J6
 Sequencing Center, Washington 4444 Forest Park Parkway, St.
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 from
 Ķ
 complete
 linear
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 6508
 Euteleostomi;
 PRI 30-SEP-2000
 Louis,
 Louis,
 Louis
 USA
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chemistry, or covered by high quality data (i.e., phred quality >30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by sequence
as compressions and repeats; all regions were covered by restriction digest.

## MAPPING INFORMATION:

The position of this clone was established as part of a collaboration between the Human Chromosome Y Mapping Project (Tomoko Kawaguchi, Helen Skaletsky, Laura G. Brown, Steve Rozen, and David C. Page at the Whitehead Institute for Blomedical Research, Cambridge MA) and the Washington University Genome Sequencing Center, St. Louis MO.

## SOURCE INFORMATION:

The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute (http://bacpac.med.buffalo.edu)

NEIGHBORING SEQUENCE INFORMATION:

The clone sequenced to the left is RP11-115H13, 200 bp overlap; the clone sequenced to the right is RP11-54OC18, 200 bp overlap. Actual start of this clone is at base position 195 of RP11-196J6; actual end is at base position 30203 of RP11-54OC18.

FEATURES

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This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate

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Consensus quality: 81125 bases at least 020
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coverage: 2.02x in 020 bases; agarose-fp
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 Direct Submission Submitted (13-JUN-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
 requests: clonerequest@sanger.ac.uk
On Aug 12, 2000 this sequence version replaced gi:9213857.
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 Plumb,B.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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7746 7845: gap of 10 bp
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 74637; con+
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FEATURES

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Insert size: 120177; 2.6% error; agarose-fp
Quality coverage: 3.57x in Q20 bases; sum-of-contigs Quality
coverage: 3.04x in Q20 bases; agarose-fp
 Submitted (09-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: hunquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Aug 25, 2000 this sequence version replaced gi:9212048.
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 Center: Sanger Centre
Center code: SC
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1. (bases 1 to 102351)
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HTG; HTGS_PHASE1; HTGS_CANCELLED
 Direct Submission
 Homo sapiens
 NOTE: This is a 'working draft' sequence. It currently consists of 10 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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10945: gap of 100 bp
22122: contig of 11177 bp in length
22222: gap of 100 bp
35055: contig of 12833 bp in length
35155: gap of 100 bp
551501 contig of 1086 bp in length
 70509:
 09: gap of
79000: con
 contig
 of
100 bp
of 8491 bp
 100 bp
f 9991 bp in length
 104
 55618
 BASE COUNT
ORIGIN
 alignment_scores:
 FEATURES
 Percent Similarity:
 98178
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 63
 Quality:
 Ratio:
 29645
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US-10-048-197-2 x AL138848
 Align seg 1/1 to: AL138848
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 98081 TGATGTGCTTAGCCAAGCACTCATAAGTGCTTAAACTATAAAACAGTTTT
 98031 GTACCAGGAGGACAAAGCTGTGGCCCGTGGGCCCACTTTGACCCCACAAATG
 35 nGlnThrIleGluGlnThrIleIleLysGlyLysThrAsnLysGln....
 19 ValThrGlyCysValSerThrGlyAsnValAlaMetLysGluGlnAsnGl 35
TCTTATTGTCTTATACCAAGCCCCCTTCTAGCACATGACTTGCTATGCATC 98227
 SerPheMetIleValValIleLysPheGlyHis.....
 79001 79100: gap of 100 bp
79101 89688: contig of 10588
89689 89788: gap of 100 bp
89789 102351: contig of 12563
 GluIleSerSerArgPheGlySerAlaAspSerIle
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89789. .10235
 70510. .79000.
/note="assembly_fragment:00869
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fragment_chain:2"
66677. .70409
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fragment_chain:2"
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1.275
57.692
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35156..50124
 /note="assembly_fragment:00700
clone_end:SP6
 vector_side:right"
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fragment_chain:1"
 /note="assembly_fragment:00779
fragment_chain:3"
 10946.
 vector_side:left"
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 /map="p32.2-33"
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 φ
 to: 102351
 Length:
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 bp in
 dq
 907
 in length
 others
 73
 62
 50
 98080
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LOCUS AL162430
 seq_name: gb_pr:AL162430
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 DEFINITION
 /ERSION
 Quality:
Ratio:
Percent Similarity:
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 JOURNAL
 TITLE
 source
 88
 74
 requests: clonerequest(sanger.ac.uk)
On Dec 4, 2000 this sequence version replaced gi:11493251.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence has been finished according to sequence map criteria
as follows. An attempt is made to resolve all sequencing problems,
such as compressions and repeats, but not necessarily within known
annotated repeat sequence elements. Where the sequence is
ambiguous, there is an annotation using the 'unsure' feature key.
The following abbreviations are used to associate primary accession
numbers given in the feature table with their source databases:
Em: EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information
on the WORMPEP database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
was generated from part of bacterial clone contigs of human
chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping
Group. Further information can be found at
http://www.sanger.ac.uk/HGP/ChrI
RP11-296A18 is from the library port-11 2 constructed.
 PheTyrLeuThr 108
 GATTTTCTGAGC 98339
 TCTACCTGAGTGGGGATTGGATCATGCCTTTTCCTCCATCATCCCTCGAT 98327
 AAGCCTCAGTGCAGGCTTCACTTCCCATCTCTGGAGTAGTTGACTGGAAC 98277
 ThrAlaIleLeuAlaProAsnArgTrpGlnGluIleLeuSerL 88
 euIleIleSerPheLeuTrpValLysProTyrArgProLysAsnLeuSer 104
 AL162430 211791 bp DNA linear PRI 30-NOV-2000 Human DNA sequence from clone RPI1-296A18 on chromosome 1, complete
 RP11-296A18 is from the library RPCI-11.2 constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong. further details see http://bacpac.med.buffalo.edu/VECTOR: pBACe3.6
 Submitted (30-NOV-2000) Sanger Centre, Hinxton, Cambridgeshire CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
 AL162430.15 GI:11544472
 AL162430
 sequence.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 Homo sapiens
 This sequence is the entire insert of clone RP11-296A18
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 (bases 1 to 211791)
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1.275
57.692
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Gaps:
Percent Identity:
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 DEFINITION
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 186719 TGATGTGCTTAGCCAAGCACTCATAAGTGCTTAAACTATAAAAACAGTTTT 186768
 186669 GTACCAGGAGGACAAAGCTGTGGCCCGTGGGCCACTTTGACCCACAAATG 186718
 JOURNAL
 186916 TCTACCTGAGTGGGGATTGGATCATGCCTTTTCCTCCATCATCCCTCGAT 186965
 186816 TCTTATTGTCTTATACCAAGCCCCTTCTAGCACATGACTTGCTATGCATC 186865
 186769 TAGTGCCTTTGGCATCATATGCTTCCCAGTTTGCCAGT...GATCCTCTT 186815
 105 PheTyrLeuThr 108
 88
 74ThrAlaIleLeuAlaProAsnArgTrpGlnGluIleLeuSerL 88
 63
 19 ValThrGlyCysValSerThrGlyAsnValAlaMetLysGluGlnAsnGl 35
 35 nGlnThrIleGluGlnThrIleIleLysGlyLysThrAsnLysGln....
 AL Submitted (27-JUN-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Jun 28, 2001 this sequence version replaced gi:14132809.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >- 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr., TREMBL; Wp:, WORMPEP; Information on the WORMPEP
 SerPheMetIleValValIleLysPheGlyHis.....
 euIleIleSerPheLeuTrpValLysProTyrArgProLysAsnLeuSer 104
 gb_pr:AL137850
 AL137850 125842 bp DNA linear PRI 27-JUN-2001
Human DNA sequence from clone RP11-56P10 on chromosome 9q31.3-33.3,
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 125842)
http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human
 SWISSPROT: Tr:, TREMBL; Wp:, WORMPEP; database can be found at
 Homo sapiens
 HTG
 complete sequence. AL137850
 Direct Submission
 Corby, N
 AL137850.12 GI:14575073
 6
 from: 1
 6
 Euteleostomi;
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FEATURES

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 source
 IMPORTANT: This sequence is not the entire insert of clone RP11-56P10 It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap. The true left end of clone RP11-4H20 is at 125743 in this sec
 chromosome 9, constructed by the Sanger Centre Chromosome Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr9 RP11-56P10 is from the library RPCI-11.1 constructed by the fleter de Jong. For further details see
 true
 //www.chori.org/bacpac/home.htm
 pBACe3.6
 right end of clone RP11-534I8
 complement(8005
 complement(1. .98)
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 12887. .13479
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 10523. .10712
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10847. .11025
 /note="MIR repeat: matches 2.
5505. .5659
 1213. .1372
/note="MIR repeat: matches 27. .191 of consensus"
 /clone="RP11-56P10"
/clone_lib="RPCI-11.1"
 'note="MIR repeat:
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 'note="AluSx repeat: matches 1.
 organism="Homo sapiens"
db_xref="taxon:9606"
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 hote="L1MC/D repeat: matches 5318.
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 repeat: matches 2089.
 repeat: matches 1.
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 .140 of consensus*
 . 231
 . 82
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 .2707
 .288 of consensus"
 .247 of consensus*
 . 58
 .2258 of consensus
 .189
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 of
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f
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 9 Mapping
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38684. .38699
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 ce="L2 repeat: matches 2267.
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 .25135
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 matches
 matches 4. .114 of consensus"
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 Em: AZ660619"
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 matches 6027.
 matches 6042.
 matches 1.
 matches
 matches
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Percent Similarity:
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 122646 T 122646
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 122432
 122620
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 4 HisHisIleArgLeuThrIleSerAlaLeuLeuThrAlaLeuLeuValTh
 AGGATGCTATGATAATCCCCATATCACAGATGAGGAAACTGAGGCTCAGA 122431
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 SerArgPheGlySerAlaAspSerIleSerPheMetIleValValIle.. 69
 AAGGTAAAATGACTTGAGAGTCAGGTAAAAGGCAGAGCCAAGATTTGAAC
 rGlyCysValSerThrGlyAsnValAlaMetLysGluGlnAsnGlnGlnT 37
 LysPheGlyHisThrA
 AC011161 200532 bp DNA linear Homo sapiens clone RP11-9L6, WORKING DRAFT SEQUENCE,
 ACO11161.3 GI:7341865
HTG; HTGS_PHASE1; HTGS_DRAFT
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 43406.
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 Length:
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 30-MAR-2000
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 COMMENT
 REFERENCE
 JOURNAL
 AUTHORS
 JOURNAL
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 Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M., Baldwin,J., Barna,N., Beckerly,R., Boguslavkiy,L., Boukhgalter,B., Brown,A., Castle,A., Colangelo,M., Collins,S., Collymore,A., Cooke,P., DeArellano,K., Dewar,K., Domino,M., Donelan,L., Doyle,M., Ferreira,P., Fitzhugh,W., Forrest,C., Funke,R., Gage,D.,
 Birren, B., Linton, L., Nusbau
Homo sapiens, clone RP11-9L6
Unpublished
 On Mar 30, 2000 this sequence version replaced gi:6139126 All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
 Direct Submission
Submitted (01-OCT-1999) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141,
 Wyman, D., Ye, W.J., Zimmer, A. and Zody, M.
 arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
 NOTE: This is a 'working draft' sequence. It currently consists of 33 contigs. The true order of the pieces is not known and their order in this sequence record is
 be preserved.
 mmalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. (bases 1 to 200532)
 (bases 1 to 200532)
 Sequencing vector: M13; M77815; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731 Consensus quality: 175452 bases at least Q40 Consensus quality: 186874 bases at least Q30 Consensus quality: 191961 bases at least Q30 Insert size: 200000; agarose-fp Insert size: 197332; sum-of-contigs
 Quality coverage: 3.2 in Q20 bases; Quality coverage: 3.2 in Q20 bases;
 Center project name: L3019
Center clone name: 9_L_6
 Contact: sequence_submissions@genome.wi.mit.edu
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 7094: contig of 1785 bp in length
7095 7194: gap of 100 bp
7195 9372: contig of 270 bp
9373 9477.
 1 1310: contig of 1310 bp in length
1311 1410: gap of 100 bp
1411 3606: contig of 2196 bp in length
 11434:
 3706:
 15643:
 7094: courty 100 bp 101 le 194: gap of 100 bp 10 le 19372: contig of 2178 bp in le 172: gap of 100 bp 11334: contig of 1862 bp in le 11434: gap of 100 bp 113848: contig of 2464 bp in le 11484: gap of 100 bp 113848: contig of 2464 bp in le 114848: contig of 24648: contig of 24
 3606: contig of 2196 b.
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19 pp of 100 bm
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13: gap of 100 bp
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 agarose-fp
sum-of-contigs
 Research
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53289; gap of
53290
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53290
54871; contig of 5637 bp in length
59027
64871; contig of 5845 bp in length
64972
70550; contig of 5845 bp in length
70551
70650; gap of
70651
70651
70632; contig of 5732 bp in length
70638
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70651
706483
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92087; gap of
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92087; gap of
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 124473 124572: gap of 100 bp
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9473. .11334
 7 29276: contig of 4120 by 7 29376: gap of 100 bp 17 29376: gap of 4538 b 7 33914: contig of 4538 b 100 bp 15 34014: gap of 100 bp 15 34014: gap of 15 770 b 15 20084: contig of 5 770 b 15 20084: con
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 .7094
 .13898
 . 5209
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 ap of 100 bp
contig of 17019 h
 contig of 17046
 100 bp
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US-10-048-197-2 x AC011161/rev
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Percent Similarity:
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 146067 AGGATGCTATGATAATCCCCATATCACAGATGAGGAAACTGAGGCTCAGA 146018
 146114 CATCAGCCCTTTTTGGAGATCTCTTTAATTATCCTAGCAATTCTC...TA 146068
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 4 HisHisIleArgLeuThrIleSerAlaLeuLeuThrAlaLeuLeuValTh
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 Submitted (28-JUL-1999) Pharmacology, West Tenth Avenue, Columbus, OH 43210, Location/Qualifiers
 3 (bases 1 to 4920)
Besco, J.A., Johnson, K.G.,
 2 (bases 1 to 4920)
Besco, J.A., Johnson, K.G., Frostholm, A., Popesco, M., Holt, C.E. and Rotter, A.
 Expression of CRYP-alpha, LAR, PTP-delta, developing xenopus visual system Mech. Dev. 92 (2), 291-294 (2000)
 Direct Submission
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 Xenopus laevis receptor protein tyrosine phosphatase Unpublished
 Johnson, K.G. and Holt, C.E.
 Xenopodinae; Xenopus.

1 (bases 1 to 4920)
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 corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em: EMBL; SW:
 Cambridgeshire, CB10 18A, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Nov 15, 2001 this sequence version replaced gi:16151438.

During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation man not be found in the sequence submission
variation annotation may not be found in the squences with
 SWISSPROT: Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 10, constructed by the Sanger Centre Chromosome 10 Mapping Group. Further information can be found at
 http://www.sanger.ac.uk/HGP/Chr10
RP11-165A20 is from the library RPCI-11.1 constructed by the group
of Pieter de Jong. For further details see
 sections only once, except for a short overlap. The true left end of clone RP11-165A20 is at 1 in this The true left end of clone RP11-80K21 is at 137492 in
 Submitted (09-NOV-2001) Wellcome Trust Sanger Institute, Hinxton Cambridgeshire, CB10 ISA, UK. E-mail enquiries:
 Homo sapiens
 complete sequence.
AL512598 AC024986
AL512598.11 GI:16944073
 AL512598 139491 bp DNA linear PRI Human DNA sequence from clone RP11-165A20 on chromosome
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 RP11-165A20 It may be shorter because we sequence overlapping
 http://www.chori.org/bacpac/home.htm
VECTOR: pBACe3.6
IMPORTANT: This sequence is not the entire insert of clone
 Ashwell.
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 AUTHORS
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Homo sapiens chromosome 11 clone RP11-711B7 map 11q23, WORKING
DRAFT SEQUENCE, 19 unordered pieces.
AP001795
 Submitted (11-APR-2000) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); Kitasato Univ., 1-15-1 Kitasato, Sagamihara, Kanagawa 228-855, Japan (E-mail:hattori@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-42-778-9923, Fax:81-42-778-9924)
On May 30, 2000 this sequence version replaced gi:7592910.
 Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y. Homo sapiens 143,873 genomic DNA of 11q23
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HTG; HTGS_PHASE1; HTGS_DRAFT.
HOMO sapiens DNA, clone:RP11-711B7.
 Quality:
 Direct Submission
 Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hon
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 143873)
 Homo sapiens
 Ratio:
Sequencing vector: PCR products; 100% of reads Chemistry: Dye-terminator ET-amersham; 100% of Assembly program: Phrap; version 0.990329 Consensus quality: 134262 bases at least Q40
 Center project name: HumDraftl1 Center clone name: RP11-711B7
 Web site: http://hgp.gsc.riken.go.jp/Contact: hattori@gsc.riken.go.jp
 Center code: RIKEN
 Center: RIKEN Genomic Sciences Center(GSC)
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 Hong-Seog, P., and Sakaki, Y.
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Sequence updated (26-May-zuvv).

* NOTE: This is a 'working draft' sequence. It currently

* consists of 19 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* arbitrary. Gaps are unknown.
 order in this sequence record is arbitrary. Gaps between the contigs are represented as runs N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
 preserved
 as soon
 NOTE: This is a 'working draft' sequence.
19 contigs. The true order of the pieces i
 This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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35205 35304: gap of 100 bp
35305 47787: contig of 12483 bp in length
47788 47887: gap of 100 bp
47888 66452: contig of 12565 bp in length
60453 60552: gap of 100 bp
60553 71377: contig of 10825 bp in length
71378 71477: gap of 100 bp
71478 83187: contig of 11710 bp in length
83188 83287: gap of 100 bp
83288 93031: contig of 9744 bp in length
 93132 101197
101198 101297:
101298 108878
 Consensus quality: 138796 bases at least Q30 consensus quality: 140745 bases at least Q20 Insert size: 142073; sum-of-contigs Quality coverage: 5.49x in Q20 bases; sum-of-contigs
 108879 108978: gap of 108979 115261: cont
 132903 134588
134589 134688:
 136969 137068:
 132803 132902:
 125188 125287: gap of 125288 130015: cont
 120165 120264: gap of 120265 125187: cont
 115262 115361:
 93032 93131:
 as it is available and the accession number will be
 134588: contig of 1686
 30115: gap of
132802: contig
 1131: gap of 100 bp
101197: contig of 8066 bp
11297: gap of 100 bp
108878: contig of 7581 bp
 7068: gap of 138355: contig
8455: gap of
140108: contig
 136968:
 3361: gap of 100 1
20164: contig of 4803
 140108
 gap of
 contig
 contig
 contig
contig
 contig
 contig
contig
 conti
 ap of 100 bp
contig of 6283 bp
 contig
 conti
 contig
 contig of 4728
 contig of 4923
 100 k
of 2687
 0f
 of 2280
 얁
 the pieces is not
 100 bp
 100 bp
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 bp in
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 bp in
 bp in
 bp in length
 bp in length
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 It currently consists of is not known and their
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 AL Submitted (19-FEB-2001) Takuji Sasaki, National Institute of Agrobiological Resources, Rice Genome Research Program; Kannondai 2-1-2; Tsukuba, Ibaraki 305-8602, Japan (E-mail:tasaski@nias.affcr.go.jp, URL:http://rgp.dna.affrc.go.jp/, Tel:81-298-38-7441, Fax:81-298-38-7468)
On Aug 9, 2001 this sequence version replaced gi:13442957.
Genes were predicted from the integrated results of the following: (October 1998 version). BLASTN2.0, BLASTN2.0 as well as SplicePredictor (October 1998 version). The genomic sequence was searched against NCBI NonRedundant protein database, nr (ftp://ncbi.nlm.nih.gov/blast/db) and the cDNA sequence database at RGP. Protein homologies of the coding regions were searched against NCBI NonRedundant protein database with BLASTR2.0 with the corresponding DDBJ accession no. and RGP clone ID. A gene with identity or significant homology to a protein but with EST protein. A gene with homology to any protein but with EST brooklogy (covering almost the entire length of partial sequence) is classified as an 'unknown' protein. A gene predicted with a gene prediction program is classified as a 'hypothetical' protein.

The orientation of the sequence is from -21M13 to M13Rev of the BAC clone. This sequence of CSJNBa0089X24 clone has an overlap with P0013F10. Detailed information on overlap and assembly quality together with annotation of this entry is available at http://rgp.dna.affrc.go.jp/GenomeSeq.html.
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 Phe 105
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 Oryza sativa genomic DNA, AP003215
 Direct Submission
 Sasaki, T., Matsumoto, T. and Yamamoto, K.
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 Oryza sativa
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 Published Only in Database (2001) In press
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a; Poales; Poaceae;
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Birren,B., Linton,L., Nusbaum,C. and Lander,E.
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 Strauss, N., Summars, M., Travers, M., willson
 Submitted (16-NOV-2001) Whitehead Institute/MIT Center Research, 320 Charles Street, Cambridge, MA 02141, USA
 Zainoun, J., Zembel
Direct Submission
 http://ftp.genome.washington.edu/RM/RepeatMasker.html
 All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
 Sequencing vector: Plasmid; n/a; 100% of reads
Sequencing vector: Plasmid; n/a; 100% of reads
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 NOTE: This is a 'working draft' sequence. It currently consists of 35 contigs. The true order of the pieces is not known and their order in this sequence record is
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 http://www-seq.wi.mit.edu
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 100 bp
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 Submitted (23-JAN-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Jul 19, 2000 this sequence version replaced gi:6731251.
All repeats were identified using RepeatMasker:
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Birren,B., Linton,L., Nusbaum,C. and Lander,E.
 * NOTE: This is a 'working draft' sequence. It currently consists of 10 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence
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Research

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Homo sapiens BAC clone RP11-298E6 from 2, complete sequence.
ACO19184
 Submitted (09-MAY-2001) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 6: On May 9, 2001 this sequence version replaced gi:7109570.
 Direct Submission
Submitted (30-DEC-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St.
MO 63108, USA
4 (bases 1 to 194372)
 3 (bases 1 to 194372) Waterston, R.H.
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Meyer,R., Maupin,R. and Bolla,S.
The sequence of Homo sapiens BAC clone RP11-298E6
 Toward a complete human genome sequence Genome Res. 8 (11), 1097-1108 (1998)
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Sulston, J.E. and Waterston, R.
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 Waterston, R.
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Mammalia; Eutheria;
 Homo sapiens
 AC019184.3 GI:14010913
Center project name: H_NH0298E06
 Contact: sapiens@watson.wustl.edu
 Center: Washington University Genome : Center code: WUGSC
Web site: http://genome.wustl.edu/gsc
 Submission
 Chordata;
Primates;
 Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
 Sequencing Center
 PRI 09-MAY-2001
 63108,
 Louis,
 USA
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NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality > 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:
Mapping information for this clone was provided by Dr. John D.
Mapping information for this clone was provided by Dr. John D.
McPherson, Department of Genetics, Washington University, St. Louis
MO. For additional information about the map position of this
sequence, see http://genome.wustl.edu/gsc

## SOURCE INFORMATION:

The RFCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., dranese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute /http://bacpac.med.buffalo.edu)
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Assembly of the database is consistent with digest information.

Location Qualifiers
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The clone sequenced to the left is RP11-194LI; the clone sequenced to the right is RP11-442O5. Actual start of this clone is at base position 1 of RP11-298E6; actual end is at base position 194372 of RP11-298E6.
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Submitted (21-APR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
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 Submitted (06-007-2001) whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Oct 6, 2001 this sequence version replaced gi:14573732. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
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 Tankka,S., Lounatmaa,K., Keranen,J., Hook,M., Westerlund-Wikstrom,B., Pouwels,P.H. and Korhonen,T.K. Characterization of the collagen-binding S-layer protein CbsA of Lactobacillus crispatus
J. Bacteriol. 182 (22), 6440-6450 (2000)
 Lactobacillus crispatus strain LMG 12003 surface layer protein (sipna) gene, complete cds.
 Submitted (06-APR-2000) IPLA-CSIC, Carretera de Infiesto s/n,
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 Submitted (19-SEP-2001) Biological Sciences, University of Alberta, CW405 Biological Sciences Bldg., Edmonton, Alta T6G 2E9, Canada
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 Direct Submission

Direct Submission

Submitted (27-APR-2000) Arabidopsis thaliana Genome Center, Submitted (27-APR-2000) Pennsylvania, 38th Street Department of Biology, University of Pennsylvania, 38th Street Department of Biology, University of Pennsylvania, 38th Street Department of Biology, University of Pennsylvania 19104-6018, USA On Jun 15, 2001 this sequence version replaced gi:7656669.

* NOTE: This is a 'working draft' sequence. It currently consists of 11 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence will
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Southwick, A., Thaveri, A., Toriumi, M., Vaysberg, M., Yu, G.,
Federspiel, N.A., Theologis, A. and Ecker, J.R.
 Arabidopsis thaliana chromosome 1 clone T28N5, *** SEQUENCING IN ACO67965
 Unpublished
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 Ecker, J.R.
 Genomic sequence for Arabidopsis thaliana BAC T28N5 from chromosome
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 thale cress.
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 AC067965.2 GI:14456635
 be preserved.
 as soon as it is available and the accession number will
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contig
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Direct Submission
Submitted (31-CCT-2000) Research Department,
Severo Ochoa 2, 28760 Tres Cantos, SPAIN
* NOTE: This is a 'working draft' sequence.
* This sequence will be replaced
* by the finished sequence as soon as it is a 'the accession number will be preserved.
 Dopazo, J., Mendoza, A., Herrero, J., Caldara, F., Pollssi, A., Humbert, Y., Friedli, L., Guerrier, M., Grand-Schenk, E., Gand Francesco, M., Buell, G., Feger, G., Garcia, E., Peitsch, M. ar
 and Garcia-Bustos, J.F.
Annotated draft genomic sequence from a Streptococcus pneumoniae type 19F clinical isolate
 Dopazo,J., Mendoza,A., Herrero,J., Caldara,F., Humbert,Y., Friedli,L., Guerrier,M., Grand-Schenk,E., Gandin,C., de Francesco,M., Polissi,A., Buell,G., Feger,G., Garcia,E., P
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 submitted (22-AUG-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA on Dec 6, 2000 this sequence version replaced gi:11276258. All repeats were identified using RepeatMasker:

Smit, A.F.A. & Green, P. (1996-1997)
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 Direct Submission
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Direct Submission
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 AC099358.2 GI:17943937
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 Norway rat.
 unpublished
 Direct Submission
 (bases 1 to 177495)
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 91
 COMMENT
 JOURNAL
 Submitted (10-NOV-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Dec 20, 2001 this sequence version replaced g1:16901764.
 findPhrapList
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NOTE: This is a 'working draft' sequence. It currently consists of 66 contigs. The true order of the pieces is not known and their order in this sequence record is
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 as soon as it is available and the accession number will be preserved.
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VERSION
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Percent Similarity:
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 119074 TTGC.....ACAGGGACACCTGGGGAGAAGGCTCCTAGTTTAAAAGTGA 119031
 67
 54
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 SerArgPhe......GlySerAlaAspSerIleSerPheMetIleVa
 lValileLysPheGly 72
 GGCCACTTCATTTTAGATTTCACCCGCGAGAGGATCTCATTCCGGGTAGT 118931
 gb_pr:AL137020
 Group. Further information can be round of the first sequence as the entire insert of clone RP11-146B14 The true left end of clone RP11-169L18 is at 151570 in this sequence. The true right end of clone RP11-403H13 is at 88099 in this sequence. This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, as follows. An attempt is made to resolve all sequencing problems.
 The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em: EMBL; Sw:, SWISSPROT; TT:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 9, constructed by the Sanger Centre Chromosome 9 Mapping Group. Further information can be found at
 requests: clonerequest@sanger.ac.uk
on Sep 11, 2000 this sequence version replaced gi:10039482.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
such as compressions and repeats, but not necessarily within known annotated repeat sequence elements. Where the sequence is ambiguous, there is an annotation using the 'unsure' feature key. RP11-146Bl4 is from the library RPCI-11.1 constructed by the group
 AL137020 182231 bp DNA linear PRI 03-JAN-2002 Human DNA sequence from clone RP11-146B14 on chromosome 9. Contains part of the gene KIAA0780, ESTs, STSs and GSSs, complete sequence.
 human.
 Direct Submission
 Babbage, A.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

[bases 1 to 182231)
 Homo sapiens
 AL137020
AL137020.13 GI:10086020
 HTG; KIAA0780.
 Quality:
 (11-JAN-2001) Sanger Centre, Hinxton, Cambridgeshire, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
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62.500
 Percent Identity:
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29.167
 21
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 of Pieter de Jong. For further details
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14989. .15042
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17636. .17681

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 complement (45910
 41889. .42199
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 32144. .32184
 complement(28428
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22510. .22813
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33021. .33313
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26758. .26797
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36281. .36579
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33452..33627
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18595. .19112
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 .2718 of consensus"
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 . 298
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US-10-048-197-2 x AL137020
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 SOURCE
ORGANISM
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 alignment_scores:
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 DEFINITION
 Align seg 1/1 to: AL137020
 Percent Similarity:
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 Norway rat.
Rattus norvegicus
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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WORKING DRAFT
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 Direct Submission
 Worley, K.C.
 Unpublished
 Elhaj,C., Escotto,M., Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Frantz,P., Gabisi,A., Gao,J., Garcia,A., Garner,T., Garzaz,N., Gill,R., Gorrell,J.H., Guevara,W., Gunarathe,P., Hale, Hamilton,K., Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A.,
 findPhrapList
 Direct Submission
 Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D.,
Consensus quality: 199000 bases at least Q40 Consensus quality: 202571 bases at least Q30 Consensus quality: 205231 bases at least Q20 Consensus quality: 205231 bases at least Q20 Estimated insert size: 199252; sum-of-contigs estimation quality coverage: 0x in Q20 bases; agarose-fp estimation Quality coverage: 4.5x in Q20 bases; sum-of-contigs estimation
 Center project name: GKEA Center clone name: CH230-
 Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
------ Project Information
 (bases 1 to 217121)
 Center code: BCM
 Assembly program: Phrap; version 0.990329First call to
 ----- Summary Statistics
 Hernandez, O., Hodgson, A., Hogues, M., Holloway, C.,
 CH230-163F6
 Edwards, C
 Hale, S.,
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TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE

JOURNAL

COMMENT

\* NOTE: Estimated insert size may differ from sequence length

\* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank.draft\_data.html).

\* NOTE: This is a 'working draft' sequence. It currently

\* NOTE: This is a 'working draft' sequence. It currently

\* consists of 35 contigs. The true order of the pieces

\* is not known and their order in this sequence record is

\* arbitrary. Gaps between the contigs are represented as

\* runs of N, but the exact sizes of the gaps are unknown.

\* This record will be updated with the finished sequence

\* as soon as it is available and the accession number will

\* be preserved. 17031 17131 34263 34363 49179 49279 17030: 17130: 34262: 34362: 0: contig of 17030 bp in length
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8: contig of 14816 bp in length
8: gap of unknown length

length

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 Results were produced by the GenCore software, Copyright (c) 1993-2000 Compugen Ltd.
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11.87
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AM352637 660033D06.x1 660 - Mi
HH160303 ENTRETSOTE RETAMOEBA hi
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HH1696 10277 Lambda-PRL2 Arabid
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Entamoeba histolytica
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Eukaryota, Entamoebidae; Entamoeba.
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Fax: 301 838 3543
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 High quality sequence start: 17 High quality sequence stop: 773.
 Email: bjloftus@tigr.org
Clones are derived from the
 Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
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AZ533627
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 Entamoeba histolytica.
Entamoeba histolytica
Eukaryota; Entamoebidae; Entamoeba.
 Contact: Brendan J Loftus
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
 genomic, DNA sequence.
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tight size distribution (-2 kb). The v + i method used for
the library construction is described in detail in Smith,
H.O. and Venter, J.C. (Making small insert libraries for
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 855 California Ave,
Tel: 650 723 2227
Fax: 650 725 8221
 Department of Biological Sciences Stanford University
 Unpublished (1999)
Contact: Walbot V
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 EST.
 mRNA sequence.
AW352637
 660033D06.x1 660 - Mixed
 University
 Walbot, V.
 Zea
 AW352637.1 GI:6851627
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 walbot@stanford.edu
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 AUTHORS
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 7 ArgLeuThrIleSerAlaLeuLeuThrAlaLeuLeuValThrGlyCysVa
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 Akimura, T., Arakawa, T., Carninci, P., Furuno, M., Hanagaki, T., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozanae, T., Imotani, K., Ishii, Y., Ito, M., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Matsuyama, T., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shinagawa, A., Shiraki, T., Sogabae, Y., Suzuki, H., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Watahiki, A., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y., Riken Encyclopedia of Mouse Full-length cDNAs (Akimura, T., et al.
Contact: Yoshihidé Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Ja
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 Mus musculus
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 BB840173
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51.485
 by Amie Franklin."
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 Email: genome-res@gsc.riken.go.jp,

URL:http://genome.gsc.riken.go.jp/

Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.

Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)

wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
 Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
 RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. . 10 (11), 1757-1771 (2000)
Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara
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Fax: 81-45-503-9216
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Fax: 650 725 8221
 Unpublished (1999)
Contact: Walbot V
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 Zea mays.
Zea mays
 946087A11.x2 946 - tassel primordium prepared by Schmidt lab Zea
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BE575116
 Stanford University
 University
 Walbot, V.
Maize ESTs from various
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 Department of Biological Sciences
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 walbot@stanford.edu
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50.000
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Fax: 650 725 8221
Email: walbot@stanford.edu
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 Unpublished (1999)
Contact: Walbot V
Department of Biological Sciences
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 Stanford University
 University
 Walbot,v.
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 Zea mays
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 CA 94304,
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Contact: Thomas Newman
MSU-DDE Plant Research Laboratory
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 Genes galore: a summary of methods for accessing results from large-scale partial sequencing of anonymous Arabidopsis cDNA clones Plant Physiol. 106, 1241-1255 (1994)
 Newman, T., deBruijn, F.J., Green, P., Keegstra, K., Kende, H., L., Ohlrogge, J., Raikhel, N., Somerville, S., Thomashow, M.,
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 E. and Somerville, C.
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 il: 22313tcn@ibm.cl.msu.edu
primer: T7 dye primer.
 139
 517-353-0854
.517-353-9168
 AAGAACTGGCAGAATGTGAGATGCCTTT 227
 AGCGTGAACTTCCTTGTTTTCCTTTTGAAG..... 255
 01190 di
a 128
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/note="Yector: lambda Zip-Lox; Site_2: Not;
/note="Yector: lambda Zip-Lox; The cDNA
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/clone="64BBT7"
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 146 g
 607 bp mRNA linear EST 07-AUG-1995
psis thaliana cDNA clone 64B8T7, mRNA
 195
 99
 164 t
 thaliana"
 30 others
 .
G
 290
 39
 Retzel
 McIntosh
 REFERENCE
AUTHORS
 VERSION
KEYWORDS
 COMMENT
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 Percent Similarity:
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JOURNAL
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 326 ACAAAGGAGAGTAAGGAGAAGATCAATGGAGAGGATGNAAGTATTCATTT
 71
 59
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 45 GlyLysThrAsnLysGlnGluIleSerSerArgPheGlySer.....
 3 AsnHisHisIleArgLeuThrIleSerAlaLeuLeuThr......
 GGNGNTATTAGGNGATACTGCATCAANTTNGCTCCTGCTNGTTGAAGGGG
 NTTTNANTGCTTTTGGGTCAATTCTTACCTTAGCG
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 .AlaLeuLeuValThrGlyCysValSer...ThrGlyAsnValAla....
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Ratio:
 אייינגליטא 745 bp mRNA linear EST 22-JAN-20
EST587236 tomato breaker fruit Lycopersicon esculentum cDNA clone
CLEG63H117 5' end, mRNA sequence.
 Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
 1 (bases 1 to 745)
Alcala,J., Vrebalov,J., White,R., Vision,T., Karamycheva,S.A., Tsi,J., Bougri,O., Kirkness,E., Utterback,T., Van Aken,S., Ronning,C.M., Fraser,C.M., Martin,G.B., Tanksley,S.D. and Giovannoni,J. Generation of ESTs from tomato fruit tissue, breaker stage (2002) Unpublished (2002)
 Lycopersicon esculentum
Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
 EST
 This clone is available through the Clemson University
 Email: http://www.genome.clemson.edu/orders/index.html
 Contact: CUGI
 BM412909.1 GI:18264539
 BM412909
 Lycopersicon.
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/cultivar="TA496"
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 Gaps:
Percent Identity:
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EST 22-JAN-2002

Genomics

275 29

BASE COUNT ORIGIN

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 heLeuTrpValLysPro 97
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 yAsnValAlaMetLysGluGlnAsnGlnGlnThrIleGluGlnThrIleI 43
 Choi.W., Fang.E., Sasinowski.M., Wing.R. and Dean.R.A. Expressed sequence characterization during appressorium formation in rice blast fungus, Magnaporthe grisea
 Magnaporthe grisea.
Magnaporthe grisea
Magnaporthe grisea
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.
 Clemson University
100 Jordan Hall, C
 mgae0002bA08f Magnaporthe grisea Appressorium Stage cDNA Library Magnaporthe grisea cDNA clone mgae0002bA08f 5', mRNA sequence.
 Clemson University Genomics Institute
 Contact: Dean, R.A.
 Unpublished (1998)
 AI068415.1 GI:3391390
 Ratio:
 (bases
 211
 864 656 5737
864 656 4293
rdean@clemson.edu
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59.551
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 VERSION
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REFERENCE AUTHORS

TITLE JOURNAL

COMMENT

J.

KEYWORDS SOURCE ORGANISM

VERSION ACCESSION DEFINITION

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75

159

60

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43 86

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 70
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 LysThrAsnLysGlnGluIleS
Lycopersicon esculentum Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; agnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
 23/ bp mRNA linear EST 18-MAY-200 EST359602 tomato fruit mature green, TAMU Lycopersicon esculentum cDNA clone cLEF56018 5', mRNA sequence.

AW933759
 EST
 AW933759.1 GI:8109160
 comato
 primer: T3 primer (AATTAACCCTCACTAAAGGG)
h quality sequence stop: 331.
 а
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237 c 227 g 201 t 12 others
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 EST 18-MAY-2001
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for 5-8
 average
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AUTHORS
KEYWORDS
SOURCE
 BASE COUNT
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JOURNAL
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 40 GlnThrIleIleLys...GlyLysThrAsnLysGlnGluIleSerSerAr
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 BI679657

370 bp mRNA linear F
949031A01.y3 949 - Juvenile leaf and shoot cDNA from
 Quality:
 Clemson University Genomics Institute Clemson University
 Unpublished (1999)
 Alcala,J., Vrebalov,J., White,R., Matern,A.L., Holt,I.E., Liang,F., Upton,J., Hansen,T., Craven,M.B., Bowman,C.L., Ahn,S., Ronning,C.M., Fraser,C.M., Martin,G.B., Tanksley,S.D. and Giovannoni,J. Generation of ESTs from tomato fruit tissue
 Zea mays cDNA,
BI679657
 5 prime sequence.
 BI679657.1 GI:15632564
 100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
 Lycopersicon
 Ratio:
 (bases 1
 mays
 160
 76.00
1.520
63.291
 pericarp"
89 c
 xhol; cLEF - Fruit were tagged at the 1cm stage and
harvested 3-5 days prior to ripening. Fruit were cut in
half to verify the seeds were indeed 'immature' and the
 /clone_11b-"tomato fruit mature green, TAMU"
/tlssue_type-"fruit pericarp"
/dev_stage-"mature green (3-5 days pre-ripening)"
/lab_host-"SOLR"
 seeds and locules were discarded prior to freezing the
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 17-SEP-2001
 BASE COUNT
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Quality:
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Percent Similarity:
 TITLE
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 University
 Walbot, V.
 Zea mays
 91
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 7 ArgLeuThrIleSerAlaLeuLeuThrAlaLeuLeuValThrGlyCysVa 23
 luGlnThrIleIleLysGlyLysThrAsnLysGlnGluIleSerSerArg
 PheGlySerAlaAspSerIleSerPheMetIleValValIleLysPheGl 72
 Email: walbot@stanford.edu
Plate: 949031 row: A column: 01.
 855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
 Department of Biological Sciences Stanford University
 Contact: Walbot
 Unpublished (1999)
 Maize ESTs from various cDNA libraries sequenced
 clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 370)
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of total RNA by weight from 4 tissue sources (see below)
were pooled, polyA+ RNA isolated, and cDNA synthesized for
EcoRI (5') and XhoI (3') directional cloning into lambda
Hybrizap vector from Stratagene. Tissue Sources: 1. Whole
shoots 3 days after sowing/imbibing in wet soil. 2. Basal
1.5 cm shoots 6 days after sowing - includes yellow
portions of developing leaves 1-5, primordia from 6-8, and
the vegetative apex. 3. Non-green portions of developing
leaves 4-5 and the vegetative apex, including adult leaf
primordia, 9 days after sowing. 4. Partially expanded and
greening leaves 4-5 at 13 days after sowing."
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Moose"
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 Percent
 Gaps:
: Identity:
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6
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 25.532
 94
 55
 226
 39
 at Stanford
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AUTHORS
TITLE
 JOURNAL COMMENT
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 39 luGlnThrIleIleLysGlyLysThrAsnLysGlnGluIleSerSerArg 55
 23 lSerThrGlyAsnValAlaMetLysGlu...GlnAsnGlnGlnThrIleG 39
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clade; Panicoideae; Andropogoneae; Zea.
 614060H04.x1 614 -
 Quality:
 Stanford University
 Contact: Walbot
 Unpublished (1999)
 Walbot, V.
Maize ESTs from various
 Zea mays.
Zea mays
 AW017581.1 GI:5871140
 mRNA sequence.
AW017581
 Email: walbot@stanford.edu
Plate: 614060 row: H col
 Department of Biological Sciences
 (bases 1 to 380)
 California Ave, Palo Alto, CA 94304, USA
 103
 650 723 2227
650 725 8221
 75.50
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50.000
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ECORI; Site_2: XhoI; 3-4 days old root tissue from Walbot
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/cultivar="W23"
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 Gaps:
Percent Identity:
 root
 80 g
 column:
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 cDNA libraries sequenced at Stanford
 from: 1
 Length:
 04.
 96 t
 mRNA
 94
4
25.532
 .
6
 linear
 257
 307
 23
 EST 13-SEP-1999
 Tracheophyta;
aceae; PACC
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alignment\_block:

Percent Similarity:

US-10-048-197-2 x BI698181

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Ratio:
 Email: walbot@stanford.edu
plate: 949031 row: A column:
Location/Qualifiers
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855 California Ave, Palo Alto,
 BI698181
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 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea
 Zea mays
 EST.
 BI698181.1 GI:15660810
 Department of Biological
 Contact: Walbot V
 Unpublished (1999)
 Maize ESTs from various cDNA libraries sequenced at Stanford
 Walbot, V.
 Zea mays.
 Zea mays cDNA, mRNA sequence.
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//notes of developing leaves 1-5, primordia from 6-8, and
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//notes of days after sowing - Partially expanded and
//notes of days after sowing - Partially expanded and
//notes of days after sowing - Including adult leaf
//notes of days after sowing - Partially expanded and
//notes of days after sowing - Including adult leaf
//notes of days after sowing - Partially expanded and
//notes of days after sowing - Partially expanded and
//notes of days after sowing - Including adult leaf
//notes of days after sowing - Partially expanded and
//notes of days after sowing - Partially expanded and
//notes of days after sowing - Including adult leaf
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//notes of days after sowing - Including adult leaf
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75.50
1.606
50.000
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AUTHORS
TITLE
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 Unpublished (1999)
Contact: Walbot V
Department of Biological Sciences
 EST.
 mRNA sequence.
AW018175
 Stanford University
855 California Ave, Palo Alto, CA 94304,
Tel: 650 723 2227
Fax: 650 725 8221
 Walbot, V.
Maize ESTs from various
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 University
 (bases 1 to 459)
 to: BI698181
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 walbot@stanford.edu
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/dev_stage="3-4 days old"
/lab_host="%LOLR"
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50.000
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 (LM)"
 ი
 from: 1
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 root
 Gaps:
Percent Identity:
 109
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CDNA
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 ខ្ល
 bp mRNA linear F
library from Walbot Lab
 450
 122 t
 80
94
4
: 25.532
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 USA
 1 others
 from Walbot Lab"
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 at Stanford
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Zea mays cDNA,
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 212 CGCCGTCGGCAACTTGGCGATGGAGGAGAAGCAGATCCAGCAGAACATCC 163
 99
 89
 39 luGlnThrIleIleLysGlyLysThrAsnLysGlnGluIleSerSerArg
 23
 72 YH1sThrAlaIleLeuAlaProAsnArgTrpGlnGluIleLeuSerLeuI 89
 56 PheGlySerAlaAspSerIleSerPheMetIleValValIleLysPheGl 72
 7 ArgLeuThrIleSerAlaLeuLeuThrAlaLeuLeuValThrGlyCysVa
 leIleSerPheLeuTrpValLysProTyrArg 99
 lSerThrGlyAsnValAlaMetLysGlu...GlnAsnGlnGlnThrIleG 39
 ACGTCAAGAGCACCATGGGGAAGCCATACAGG
 Email: walbot@stanford.edu
Plate: 606069 row: H colum
Location/Qualifiers
 855 California Ave, Palo
Tel: 650 723 2227
Fax: 650 725 8221
 Unpublished (1999)
Contact: Walbot V
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.
 Zea mays
 606069H03.x1 606 - Ear tissue
 Walbot, V.
Maize ESTs from various cDNA libraries
 EST.
 AI834558.1 GI:5468767
 mays cDNA, mRNA sequence.
 Stanford University
 Department of Biological Sciences
 University
 Zea mays.
 (bases 1 to 460)
 119
 AAGAACTGGCAGAATGTGAGATGCCTCT 100
 /dev_stage="ear length from 0.5 cm - 2.0 cm"
/lab_host="XLOLR (Stratagene)"
/note="Organ: immature ear; Vector: pBK-CMV; Site_1: EcoRI; Site_2: XhoI; Mixed ear tissue cDNA library from Schmidt lab"
 /organism="Zea mays"
/cultivar="0hio43"
/db_xref="Laxon:4577"
/clone_lib="606 - Ear tissue cDNA library from Schmidt
 /tissue_type="mixed"
 AGCGTGAACTTCCTTGTTTCCCTTCTGAAG....
 o
 97
 column:
 Alto,
 460 bp
 ø
 from: 1 to: 459
 CDNA
 89
 CA 94304,
 ၀
 mRNA linea
library from
```

linear

ar EST 02-FEB-2000 Schmidt lab Zea

128

55

23

158

sequenced

at

Stanford

USA

```
alignment_block:
US-10-048-197-2 x AI834558/rev
 FEATURES
 alignment_scores:
 COMMENT
 REFERENCE
 seq_documentation_block:
LOCUS BI245316
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 VERSION
 ACCESSION
 DEFINITION
 SOURCE
 KEYWORDS
 Align seg 1/1 to reverse of: AI834558
 Percent Similarity:
 TITLE
 AUTHORS
 ORGANISM
 JOURNAL
 source
 295
 300
 350
 397
 237 ACGTCAAGAGCACCATGGGGAAGCCATACAGG 206
 39
 89
 72
 56 PheGlySerAlaAspSerIleSerPheMetIleValValIleLysPheGl 72
 23 lSerThrGlyAsnValAlaMetLysGlu...GlnAsnGlnGlnThrIleG 39 |:::::::||||||:::|||:
 yHisThrAlaIleLeuAlaProAsnArgTrpGlnGluIleLeuSerLeuI 89
 luGlnThrIleIleLysGlyLysThrAsnLysGlnGluIleSerSerArg 55
 AGATG.....
 CGCCGTCGGCAACTTGGCGATGGAGGAGGAGCAGCAGCAGCAGCATCC 301
 AAGGCAACCGTCAAGTTCCAGCTCAAGAAGGTCCTTTGCATGGGC...GT 351
 ArgLeuThrIleSerAlaLeuLeuThrAlaLeuLeuValThrGlyCysVa 23
 leIleSerPheLeuTrpValLysProTyrArg
 AAGAACTGGCAGAATGTGAGATGCCTTT 238
 AGCGTGAACTTCCTTGTTTCCCTTCTGAAG.....
 Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA
Tel: 650 723 227
Fax: 650 725 8221
 Email: walbot@stanford.edu
Plate: 949031 row: A column:
 Contact: Walbot
 Unpublished (1999)
 Maize ESTs from various cDNA libraries sequenced at Stanford
 Walbot, V.
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.
 BI245316
BI245316.1 GI:14717666
 HI245316 467 bp ml 949031A01.x2 949 - Juvenile leaf and
 Quality:
 University
 Zea mays
 Zea mays cDNA, mRNA sequence.
 Ratio:
 (bases 1
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/cultivar="W64A"
/db_xref="taxon:4577"
/clone_lib="949 - Juver
 /tissue_type="immature leaf primordium and vegetative
meristem"
 75.50
1.606
50.000
/dev_stage="4 stages from 3–13 days after imbibing"
/lab_host="E. coli XLOLR"
 ocation/Qualifiers
 ç
 Percent
 Length:
Gaps:
Identity:
 Juvenile leaf and shoot cDNA from Steve
 from: 1
 99
 CA 94304, USA
 01
 mRNA
 RNA linear I
shoot cDNA from
 25
 to:
 94
 460
 EST 13-JUL-2001
m Steve Moose
 REFERENCE
AUTHORS
TITLE
 KEYWORDS
SOURCE
ORGANISM
 seq_name: gb_est2:BE511166
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US-10-048-197-2 x BI245316
 alignment_scores:
Quality:
 BASE COUNT
ORIGIN
 COMMENT
 DEFINITION
 seq_documentation_block:
 ACCESSION
 VERSION
 Align seg 1/1 to: BI245316
 Percent Similarity:
 JOURNAL
 261
 289 ACGTCAAGAGCACCATGGGGAAGCCATACAGG
 89 lelleSerPheLeuTrpValLysProTyrArg 99
 72 yHisThrAlaIleLeuAlaProAsnArgTrpGlnGluIleLeuSerLeuI 89
 AAGAACTGGCAGAATGTGAGATGCCTCT 288
 946058002.x1 946 - tassel primordium prepared by Schmidt lab Zea BE511166
 Unpublished (1999)
Contact: Walbot V
Department of Biological Sciences
Stanford University
 Eukaryota; Viridiplantae; Streptophyta; Em
Spermatophyta; Magnoliophyta; Liliopsida;
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 488)
 Walbot, V.
 Zea mays
 EST
 BE511166.1 GI:9732414
 University
 Maize ESTs from various
 Zea mays.
 Ratio:
 116
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cDNA libraries

sequenced

at Stanford

Embryophyta; Tracheophyta; a; Poales; Poaceae; PACC

(

```
231AGCGTGAACTTCCTTGTTTCCCTTCTGAAG.....
 226 AGATG.....
 176 CGCCGTCGGCAACTTGGCGATGGAGGAGGAAGCAGCAGCAGAACATCC
 129 AAGGCAACCGTCAAATTCCAGCTCAAGAAGGTCCTTTGCATGGGC...
 56 PheGlySerAlaAspSerIleSerPheMetIleValValIleLysPheGl 72
 23 | SerThrGlyAsnValAlaMetLysGlu...GlnAsnGlnGlnThrIleG 39
 39 luGlnThrIleIleLysGlyLysThrAsnLysGlnGluIleSerSerArg
 7 ArgLeuThrIleSerAlaLeuLeuThrAlaLeuLeuValThrGlyCysVa ::: |||::::: ||| || || || ||
 /note="Organ: juvenile vegetative shoots; Vector:
pAD-GAL4-2.1; Site_1: EcoRI; Site_2.2: Nho1; Equal amounts
of total RNA by weight from 4 tissue sources (see below)
were pooled, polyh+ RNA isolated, and cDNA synthesized for
EcoRI (5') and XhoI (3') directional cloning into lambda
Hybrizap vector from Stratagene. Tissue Sources: 1. Whole
shoots 3 days after sowing/imbibing in wet soil. 2. Basal
1.5 cm shoots 6 days after sowing in vector from 5. Since the vegetative apex. 3. Non-green portions of developing
leaves 4-5 and the vegetative apex, including adult leaf
primordia, 9 days after sowing. 4. Partially expanded and
greening leaves 4-5 at 13 days after sowing."
 75.50
1.606
50.000
 from: 1
 Percent
 Length: 94
Gaps: 4
t Identity: 25.532
 to: 467
 .GT 175
 55
 23
 230
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US-10-048-197-2 x BE511166/rev
 SOURCE
ORGANISM
 ACCESSION
VERSION
 alignment_scores:
 BASE COUNT
 FEATURES
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 DEFINITION
 seq_documentation_block:
 KEYWORDS
 Align seg 1/1 to reverse of: BE511166
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 244
 249
 source
 299 CGCCGTCGGCAACTTGGCGATGGAGGAGGAAGCAGCAGATCCAGCAGAACATCC
 346 AAGGCAACCGTCAAGTTCCAGCTCAAGAAGGTCCTTTGCATGGGC...GT 300
 9
 56
 39 luGlnThrIleIleLysGlyLysThrAsnLysGlnGluIleSerSerArg
 72 yH1sThrAlaIleLeuAlaProAsnArgTrpGlnGluIleLeuSerLeuI 89
 7 ArgLeuThrIleSerAlaLeuLeuThrAlaLeuLeuValThrGlyCysVa
 ACGTCAAGAGCACCATGGGGAAGCCATACAGG 155
 leIleSerPheLeuTrpValLysProTyrArg 99
 PheGlySerAlaAspSerIleSerPheMetIleValValIleLysPheGl 72
 Zea mays.
Zea mays
 Zea mays cDNA, mRNA
BI431074
 Quality:
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.
 BI431074.1 GI:15214850
EST.
 BI431074 491 bp mRNA linear F
949069B08.x1 949 - Juvenile leaf and shoot cDNA from
 Tel: 650 723 2227 Fax: 650 725 8221
 Plate:
 Ratio:
 California Ave, Palo Alto, CA 94304, USA
 129
 946058 row: D column:
Location/Qualifiers
 walbot@stanford.edu
 ø
 75.50
1.606
50.000
 between 1mm and 3mm. Sharon Stanfield p
library in HybriZaP. Sample insert size
to 3 Kb with a 1 Kb average."
121 c 116 g 122 t
 /note="Organ: tassels; Vector: HybriZAP; Site_1: EcoRI;
Site_2: xhoI; George Chuck dissected immature tassels
 /dev_stage="just after the transition from vegetative
inflorescence development"
 /organism="Zea mays"
/cultivar="0443"
/db_xref="faxon:4577"
/clone_11b="946 - tassel primordium prepared by Schmidt
 /lab_host-"XLOLR"
 'tissue_type="tassels"
 . 488
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 AAGAACTGGCAGAATGTGAGATGCCTCT
 Gaps:
Percent Identity:
 from: 1
 Length:
 2
 94
4
25.532
 8
 Stanfield prepared the cDNA
 245
 55
 250
 39
 range was 350 bp
 EST 20-AUG-2001
 Steve Moose
 FEATURES
 COMMENT
 JOURNAL
 201
 256
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US-10-048-197-2 x BI431074/rev
 alignment_scores:
 BASE COUNT
 REFERENCE
 Align seg 1/1 to reverse of: BI431074 from: 1
 Percent Similarity:
 AUTHORS
TITLE
 303 AAGGCAACCGTCAAATTCCAGCTCAAGAAGGTCCTTTGCATGGGC...GT
 source
 206 AGATG.....
89 leIleSerPheLeuTrpValLysProTyrArg ::::::
 23 lSerThrGlyAsnValAlaMetLysGlu...GlnAsnGlnGlnThrIleG
 39 luGlnThrIleIleLysGlyLysThrAsnLysGlnGluIleSerSerArg
 7 ArgLeuThrIleSerAlaLeuLeuThrAlaLeuLeuValThrGlyCysVa
 AGCGTGAACTTCCTTGTTTCCCTTCTGAAG.....
 PheGlySerAlaAspSerIleSerPheMetIleValValIleLysPheGl
 CGCCGTCGGCAACTTGGCGATGGAGGAGAAGCAGATCCAGCAGAACATCC
 yHisThrAlaIleLeuAlaProAsnArgTrpGlnGluIleLeuSerLeuI 89
 855 California Ave,
Tel: 650 723 2227
Fax: 650 725 8221
 Unpublished (1999)
Contact: Walbot V
 1 (bases 1 to 491)
Walbot, V.
Maize ESTs from various
 Quality:
 Plate: 949069 row: B
 Email: walbot@stanford.edu
 Stanford University
 Department of Biological Sciences
 University
 Ratio:
 121
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//lab_host="E. coli XLOLR"
//lab_host="E. coli XLOLR"
//note="Organ: juvenile vegetative shoots; Vector:
pAD-GAL4-2.1, Site_1: EcoRI; Site_2: XhoI; Equal amounts
of total RNA by weight from 4 tissue sources (see below)
were pooled, polyA+ RNA isolated, and cloNA synthesized for
EcoRI (5') and XhoI (3') directional cloning into lambda
Hybrizap vector from Stratagene. Tissue Sources: 1. Whole
shoots 3 days after sowing/imbibing in wet soil. 2. Basal
1.5 cm shoots 6 days after sowing includes yellow
portions of developing leaves 1-5, primordia from 6-8, and
the vegetative apex. 3. Non-green portions of developing
leaves 4-5 and the vegetative apex, including adult leaf
primordia, 9 days after sowing. 4. Partially expanded and
greening leaves 4-5 at 13 days after sowing."
 /tissue_type="immature leaf primordium
meristem"
 Moose"
 75.50
1.606
50.000
 /db_xref="taxon:4577"
/clone_lib="949 - Juvenile leaf and shoot cDNA from Steve
 /organism="Zea mays"
/cultivar="W64A"
 9069 row: B column:
Location/Qualifiers
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 Percent Identity:
 Palo Alto, CA 94304, USA
 cDNA libraries sequenced at Stanford
 Length:
 99
 80
 94
4
25.532
 to: 491
 and
 144
 172
 55
 39
 23
 72
 207
 257
 202
 vegetative
```

```
BASE COUNT
ORIGIN
 SOURCE
ORGANISM
 REFERENCE
AUTHORS
 VERSION
KEYWORDS
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US-10-048-197-2 x AW037170
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 DEFINITION
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 ACCESSION
 Align seg 1/1 to: AW037170
 Ratio:
Percent Similarity:
 TITLE
 JOURNAL
 256
 251
 201
 154
 source
 143
 56
 39 luGlnThrIleIleLysGlyLysThrAsnLysGlnGluIleSerSerArg
 23
 72 yHisThrAlaIleLeuAlaProAsnArgTrpGlnGluIleLeuSerLeuI 89
 PheGlySerAlaAspSerIleSerPheMetIleValValIleLysPheGl 72
 AGCGTGAACTTCCTTGTTTCCCTTCTGAAG.....
 AAGGCAACCGTCAAGTTCCAGCTCAAGAAGGTCCTTTGCATGGGC...GT 200
 CGCCGTCGGCAACTTGGCGATGGAGGAGGAAGCAGATCCAGCAGAACATCC
 lSerThrGlyAsnValAlaMetLysGlu...GlnAsnGlnGlnThrIleG 39
 ArgLeuThrIleSerAlaLeuLeuThrAlaLeuLeuValThrGlyCysVa
 ACGTCAAGAGCACCATGGGGAAGCCATACAGG
 gb_est1:AW037170
 Zea mays.
Zea mays
 Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 8227
Fax: 650 725 8221
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 492)
 Quality:
 614018H02.y1 614 -
 Contact: Walbot V
 Unpublished (1999)
 University
 Maize ESTs from various cDNA libraries sequenced
 Walbot, V.
 AW037170.1 GI:5895924
 mRNA sequence.
 Plate: 614018 row: H column
Location/Qualifiers
 Department of Biological Sciences
 124
 walbot@stanford.edu
 D
 /vigue_11D="614 - root cDNA library from Walbot /tissue_type="root" /dev_stage="3-4 days old" /lab host="wvcvr"
 75.50
1.606
50.000
 Lab
 EcoRI; Site_2: XhoI; 3-4 days
 /note="Organ:
 /db_xref="taxon:4577"
/clone_lib="614 - root
 /organism="Zea mays"
/cultivar="W23"
 /lab_host="XLOLR"
 ი
 from: 1
 root
Percent
 125
 root; Vector:
 column: 02
 CDNA
 g
 Length:
Gaps:
Identity:
 to: 492
 bp mRNA
library from
 112
 126 t
 94
4
25.532
 RNA linear E
from Walbot Lab
 pBlueScriptII SK+; Site_1:
ys old root tissue from Walbot
 1 others
 55
 255
 250
 23
 at Stanford
 EST 15-SEP-1999
b Zea mays cDNA,
```

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alignment_block:
US-10-048-197-2 x BI478440
 JOURNAL
COMMENT
 SOURCE
ORGANISM
 BASE COUNT
ORIGIN
 ACCESSION
VERSION
 alignment_scores:
 FEATURES
 seq_documentation_block:
LOCUS
 seq_name:
 REFERENCE
 DEFINITION
 KEYWORDS
 Ratio:
Percent Similarity:
 Align seg 1/1 to: BI478440
 AUTHORS
TITLE
 source
 286
 314 ACGTCAAGAGCACCATGGGGAAGCCATACAGG 345
 9
7 ArgLeuThrIleSerAlaLeuLeuThrAlaLeuLeuValThrGlyCysVa
 leIleSerPheLeuTrpValLysProTyrArg 99
 AAGAACTGGCAGAATGTGAGATGCCTCT 313
 gb_est2:BI478440
 Quality:
 855 California Ave,
Tel: 650 723 2227
Fax: 650 725 8221
 Zea mays.
Zea mays.
 Department of Biological Stanford University
 Zea mays cDNA, mRNA sequence.
BI478440
BI478440.1 GI:15312868
 BI478440 512 bp mRNA linear EST 27-AUG-2001 949069B08.yl 949 - Juvenile leaf and shoot cDNA from Steve Moose
 Unpublished (1999)
 University
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
 EST.
 Contact: Walbot
 Maize ESTs from various cDNA libraries sequenced
 Walbot,V
 clade; Panicoideae; Andropogoneae;
1 (bases 1 to 512)
 139
 949069 row: B
 walbot@stanford.edu
 Ø
 /organism="Zea mays"
/cultivar="W64A"
/db_xref="taxon:4577"
/clone_lib="949 - Juven
 Hybrizap vector from Stratagene. Tissue Sources: 1. Whole shoots 3 days after sowing/imbibing in wet soil. 2. Basal 1.5 cm shoots 6 days after sowing - includes yellow portions of developing leaves 1-5, primordia from 6-8, and the vegetative apex. 3. Non-green portions of developing leaves 4-5 and the vegetative apex, including adult leaf primordia, 9 days after sowing. 4. Partially expanded and greening leaves 4-5 at 13 days after sowing. **
 /lab_host="E. coli XLOLR"
/note="Organ: juvenile vegetative shoots; Vector:
/note="Organ: juvenile vegetative shoots; Vector:
pAD-GAL4-2.1; Site_1: EcoRI; Site_2: XhoI; Equal amounts
of total RNA by weight from 4 tissue sources (see below)
were pooled, polyA+ RNA isolated, and cDNA synthesized for
were pooled, polyA+ RNA isolated, and cDNA synthesized for
EcoRI (5') and XhoI (3') directional cloning into lambda
 75.50
1.606
50.000
 greening leaves 4-5 at 13 days after
 /tissue_type="immature leaf primordium and vegetative
meristem"
 /dev_stage="4 stages from 3-13 days after imbibing"
/lab_host="E coli XLOLR"
 location/Qualifiers
 122 c
 from:
 Length:
Gaps:
Percent Identity:
 Palo Alto,
 126 g
 column:
 سا
 Sciences
 to:
 Juvenile leaf and shoot cDNA from
 512
 CA 94304,
 80
 94
4
25.532
 USA
 23
 at Stanford
 Steve
```

```
BASE COUNT
ORIGIN
 JOURNAL COMMENT
 REFERENCE
AUTHORS
 SOURCE
ORGANISM
 alignment_block:
US-10-048-197-2 x AW171836/rev
 ACCESSION
VERSION
 seq_documentation_block:
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 KEYWORDS
 DEFINITION
 Percent Similarity:
Align seg 1/1
 TITLE
 245
 195
 source
 308 ACGTCAAGAGCACCATGGGGAAGCCATACAGG 339
 148
 89
 72 yH1sThrAlaIleLeuAlaProAsnArgTrpGlnGluIleLeuSerLeuI 89
 56 PheGlySerAlaAspSerIleSerPheMetIleValValIleLysPheGl 72
 39 luGlnThrIleIleLysGlyLysThrAsnLysGlnGluIleSerSerArg 55
 23 lSerThrGlyAsnValAlaMetLysGlu...GlnAsnGlnGlnThrIleG 39
 leIleSerPheLeuTrpValLysProTyrArg 99
 CGCCGTCGGCAACTTGGCGATGGAGGAGAAGCAGATCCAGCAGAACATCC
 AAGGCAACCGTCAAATTCCAGCTCAAGAAGGTCCTTTGCATGGGC...GT 194
 AAGAACTGGCAGAATGTGAGATGCCTCT
 AGCGTGAACTTCCTTGTTTCCCTTCTGAAG.....
 sequence.
AW171836
 Quality:
 855 California Ave, Palo Alto, CA 94304,
Tel: 650 723 2227
Fax: 650 725 8221
 Department of Biological Sciences Stanford University
 Contact: Walbot
 Unpublished (1999)
 Walbot, V.
Maize ESTs from various cDNA libraries sequenced at Stanford
 clade; Panicoideae; Andropogoneae;
l (bases 1 to 513)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
 Zea mays.
 618051B11.x1 618 - Inbred
 AW171836.1
 Email: walbot@stanford.edu
Plate: 618051 row: B col
 Ratio:
 to reverse of: AW171836
 114
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Inbred tassel library from Schmidt lab"
137 c 128 g 134 t
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/clone_lib="618 - Inbred Tassel cDNA Library"
/tissue_type="tassel"
/dev_stage="tassel length from 0.1 to 2.5 cm"
/lab_host="XLOLR"
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1.606
50.000
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/cultivar="Ohio43"
 Location/Qualifiers
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Gaps:
Percent Identity:
 column:
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 from: 1
 11.
 Zea.
 94
4
25.532
.
6
 USA
 513
 244
 279
 249
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JOURNAL
COMMENT
 REFERENCE
AUTHORS
 BASE COUNT
ORIGIN
 VERSION
KEYWORDS
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 DEFINITION
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 ACCESSION
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 ORGANISM
 143
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 138
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 56
 80
 89
 23
 72 yHisThrAlaIleLeuAlaProAsnArgTrpGlnGluIleLeuSerLeuI 89
 39 luGlnThrIleIleLysGlyLysThrAsnLysGlnGluIleSerSerArg
 PheGlySerAlaAspSerIleSerPheMetIleValValIleLysPheGl 72
 ArgLeuThrIleSerAlaLeuLeuThrAlaLeuLeuValThrGlyCysVa
::: ||||::::: |||
 ACGTCAAGAGCACCATGGGGAAGCCATACAGG
 leIleSerPheLeuTrpValLysProTyrArg 99
 lSerThrGlyAsnValAlaMetLysGlu...GlnAsnGlnGlnThrIleG 39
 Quality:
Ratio:
 mays cDNA, mRNA sequence.
AI586595
 486049C06.x4 486 - leaf primordia
 Zea mays
 Email: walbot@stanford.edu
Plate: 486049 row: C column: 06.
Location/Qualifiers
 Stanford University
855 California Ave, Palo Alto,
Tel: 650 723 227
Fax: 650 725 8221
 Contact: Walbot V
 Unpublished (1999)
 Maize ESTs from various cDNA libraries sequenced
 Walbot, V.
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoldeae; Andropogoneae; Zea
 Zea mays.
 AI586595.1 GI:4572946
 Department of Biological Sciences
 (bases 1 to 514)
 138
 library."
123 c
75.50
1.606
50.000
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/dev_stage="p7-p11 leaf"
/lab_host="E.coli XL1-Blue MFR'"
 /db_xref="taxon:4577"
/clone_lib="486 - lea
 /organism="Zea mays"
/cultivar="B73"
 'note="Organ: shoot; Vector:
 .AGCGTGAACTTCCTTGTTTCCCTTCTGAAG..... 109
 o
 113 g
 514 bp
 leaf primordia
 Length:
 CA
 140
 mRNA linear
cDNA library from
 94304, USA
 Lambda zap; Hake
 94
 CDNA
 library
 55
 23
 at
 Stanford
 EST 07-APR-1999
Hake lab Zea
 lab
 from
 CDNA
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Percent Similarity:

Percent Identity:

25.532

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JOURNAL COMMENT
 REFERENCE
AUTHORS
 SOURCE
ORGANISM
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US-10-048-197-2 x AI586595/rev
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 seq_documentation_block:
 KEYWORDS
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 Align seg 1/1 to reverse of: AI586595
 TITLE
 source
 216
 274
 279
 329 TGCCGTTGGCAACTTGGCGATGGAGGAGGAGCAGCAGCAGCAGCATCC
 376 AAGGCAACCGTCAAGTTCCAGCTCAAGAAGGTTCTTTGCATGGGT...GT
٠
 72 yHisThrAlaIleLeuAlaProAsnArgTrpGlnGluIleLeuSerLeuI
 56 PheGlySerAlaAspSerIleSerPheMetIleValValIleLysPheGl 72
 39 luGlnThrIleIleLysGlyLysThrAsnLysGlnGluIleSerSerArg
 23
 leIleSerPheLeuTrpValLysProTyrArg 99
 AGATG.....
 lSerThrGlyAsnValAlaMetLysGlu...GlnAsnGlnGlnThrI1eG
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 gb_est2:BI643532
 855 California Ave, Palo Alto,
Tel: 650 723 2227
Fax: 650 725 8221
 Unpublished (1999)
Contact: Walbot V
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.
 Zea mays cDNA, mRNA sequence.
BI643532
 BI643532 518 bp mRNA linear F
949079C10.xl 949 - Juvenile leaf and shoot cDNA from
 Email: walbot@stanford.edu
Plate: 949079 row: C col
 Stanford University
 Department of Biological Sciences
 University
 Maize ESTs from various cDNA libraries sequenced at Stanford
 Zea mays
 Zea mays.
 BI643532.1 GI:15545738
 (bases 1 to 518)
 /note="Organ: juvenile vegetative shoots; Vector: pAD-GAL4-2.1; Site_1: EcoRI; Site_2: XhoI; Equal amounts of total RNA by weight from 4 tissue sources (see below) were pooled, polyA+ RNA isolated, and cDNA synthesized for EcoRI (5') and XhoI (3') directional cloning into lambda Hybrizap vector from Stratagene. Tissue Sources: 1. Whole
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/clone_lib="949 - Juvenile leaf and shoot cDNA from Steve
Moose"
 /tissue_type="immature leaf primordium and vegetative meristem" % \left(\frac{1}{2}\right) =\frac{1}{2}\left(\frac
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 organism="Zea mays"
cultivar="W64A"
 Location/Qualifiers
 AGCGTCAACTTCCTTGTTTCCCTTCTGAAG.....
 .AAGAACTGGCAGAATGTGAGATGCCTCT 217
 column:
 from: 1
 10
 CA 94304, USA
 ;
6
 89
 245
 55
 280
 39
 330
 275
 23
 imbibing"
 EST 10-SEP-2001
 Steve Moose
 REFERENCE
AUTHORS
 SOURCE
ORGANISM
 COMMENT
 seq_documentation_block:
 seq_name:
 alignment_scores:
 ORIGIN
 FEATURES
 KEYWORDS
 DEFINITION
 BASE COUNT
 VERSION
 ACCESSION
 Percent Similarity:
 JOURNAL
 TITLE
 198
 226
 256
 261
 311
 72
 56
 EST.
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 23 lSerThrGlyAsnValAlaMetLysGlu...GlnAsnGlnGlnThrIleG |::::::||||||:::||| ||| |||||:::|||:
 89 lelleSerPheLeuTrpValLysProTyrArg
 39 luGlnThrIleIleLysGlyLysThrAsnLysGlnGluIleSerSerArg
 7 ArgLeuThrIleSerAlaLeuLeuThrAlaLeuLeuValThrGlyCysVa
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 AGCGTGAACTTCCTTGTTTCCCTTCTGAAG.....
 PheGlySerAlaAspSerIleSerPheMetIleValValIleLysPheGl
 gb_est1:AI629856
 Stanford University
855 California Ave, Palo
Tel: 650 723 2227
Fax: 650 725 8221
 Unpublished (1999)
Contact: Walbot V
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.
 mays cDNA, mRNA sequence.
AI629856
 A1629856 529 bp
486041B10.x2 486 - leaf primordia
 Zea mays
 Quality:
 Plate: 486041
 Department of Biological Sciences
 University
 Walbot, V
 Zea mays.
 AI629856.1 GI:4681186
 Email: walbot@stanford.edu
 Maize ESTs from various
 Ratio:
 (bases 1 to 529)
 138
 Ø
 shoots 3 days after sowing/imbibing in wet soil. 2. Basal 1.5 cm shoots 6 days after sowing - includes yellow portions of developing leaves 1-5, primordia from 6-8, and the vegetative apex. 3. Non-green portions of developing leaves 4-5 and the vegetative apex, including adult leaf primordia, 9 days after sowing. 4. Partially expanded and greening leaves 4-5 at 13 days after sowing."
16041 row: B column: Location/Qualifiers
 75.50
1.606
50.000
 .AAGAACTGGCAGAATGTGAGATGCCTCT 199
 Percent Identity:
 cDNA libraries sequenced at Stanford
 Alto,
 99
 167
 CA 94304,
 10
 cDNA library from
 94
4
25.532
 .
6
 USA
 linear
 227
 55
 39
 312
 257
 23
 Hake lab Zea
 EST 26-APR-1999
 6-8, and
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REFERENCE
AUTHORS
TITLE
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US-10-048-197-2 x AI629856/rev
 BASE COUNT
ORIGIN
 SOURCE
ORGANISM
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 COMMENT
 seq_documentation_block:
 ACCESSION
 DEFINITION
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 KEYWORDS
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 Percent Similarity:
 Align seg 1/1 to reverse of: AI629856
 JOURNAL
 300 AGATG.....
 397
 295
 source
 237
 72 yHisThrAlaIleLeuAlaProAsnArgTrpGlnGluIleLeuSerLeuI 89
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 39 luGlnThrIleIleLysGlyLysThrAsnLysGlnGluIleSerSerArg 55
 leIleSerPheLeuTrpValLysProTyrArg 99
 AAGGCAACCGTCAAGTTCCAGCTCAAGAAGGTTCTTTGCATGGGT...GT 351
 ACGTCAAGAGCACCATGGGGAAGCCATACAGG
 AGCGTCAACTTCCTTGTTTCCCTTCTGAAG..... 266
 ArgLeuThrIleSerAlaLeuLeuThrAlaLeuLeuValThrGlyCysVa
Unpublished (1999)
Contact: Walbot V
Department of Biological Sciences
Stanford University
B55 California Ave, Palo Alto, CA 94304, USA
 Zea mays.

Zea mays

Lea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Eukaryota; Varidiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC

clade; Panicoldeae; Andropogoneae; Zea.
 Zea mays cDNA, mRNA sequence.
BI180391
 BI180391 533 bp mRNA 949031A01.x1 949 - Juvenile leaf and shoot
 University
 BI180391.1 GI:14646202
 Malze ESTs from various cDNA libraries sequenced at Stanford
 Ratio:
 (bases 1 to 533)
 142
 ø
 75.50
1.606
50.000
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/cultlvar="873"
/db_xref="taxon:4577"
/clone_lib="486 - leaf primordia cDNA library from Hake lab"
 library."
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/dev_stage="P7-P11 leaf"
/lab_host="E.coli xl1-Blue MFR'"
/note="Organ: shoot; Vector: Lambda
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 126 c
 Percent
 114 g
 Identity:
 from: 1 to:
 206
 147 t
 94
4
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 cDNA from Steve
 linear
 zap;
 296
 23
 Hake lab
 EST 09-JUL-2001
 Moose
 CDNA
```

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US-10-048-197-2 x BI180391/rev
 BASE COUNT
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 FEATURES
 ACCESSION
 DEFINITION
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 Align seg 1/1 to reverse of: BI180391
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 267
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 204 ACGTCAAGAGCACCATGGGGAAGCCATACAGG
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 23 lSerThrGlyAsnValAlaMetLysGlu...GlnAsnGlnGlnThrIleG 39
 56 PheGlySerAlaAspSerIleSerPheMetIleValValIleLysPheGl 72
 72 yHisThrAlaIleLeuAlaProAsnArgTrpGlnGluIleLeuSerLeuI 89
 7 ArgLeuThrIleSerAlaLeuLeuThrAlaLeuLeuValThrGlyCysVa
 AGATG.....
 leIleSerPheLeuTrpValLysProTyrArg
 AGCGTGAACTTCCTTGTTTCCCTTCTGAAG.....
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 mRNA sequence.
AW090901
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AW090901.1 GI:6056511
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 Fax: 650 725 8221
 Ratio:
 142
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//dev_stage="4 stages from 3-13 days after imbibing"
//dev_stage="6" coli XLOLR"
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//note="Organ: juvenile vegetative shoots; Vector:
//note="Organ: juvenile received; Site_2: XhoI; Equal amounts
of total RNA by weight from 4 tissue sources (see below)
were pooled, polyA+ RNA isolated, and CDNA synthesized for
ECORI (5') and XhoI (3') directional cloning into lambda
Hybrizap vector from Stratagene. Tissue Sources: 1. Whole
shoots 3 days after sowing/imbibing in wet soil. 2. Basal
1.5 cm shoots 6 days after sowing includes yellow
portions of developing leaves 1-5, primordia from 6-8, and
the vegetative apex. 3. Non-green portions of developing
leaves 4-5 and the vegetative apex, including adult leaf
primordia, 9 days after sowing. 4. Partially expanded and
greening leaves 4-5 at 13 days after sowing. "
42 a 133 c 124 g 134 t
 walbot@stanford.edu
949031 row: A colu
 /db_xref="taxon:4577"
/clone_lib="949 - Juve
Moose"
 /tissue_type="immature leaf primordium and vegetative meristem" % \left(\frac{1}{2}\right) =\frac{1}{2}\left(\frac
 75.50
1.606
50.000
 cultivar="W64A"
 organism="Zea mays"
 Location/Qualifiers
 root cDNA
 Gaps:
Percent Identity:
 :
 column:
 Juvenile leaf and shoot cDNA from Steve
 from: 1
 bp mRNA
library from
 173
 99
 요
:
 94
4
25.532
 .
6
 linear F
Walbot Lab
 233
 268
 EST 18-OCT-1999
Zea mays cDNA,
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US-10-048-197-2 x AW090901
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 KEYWORDS
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 COMMENT
 REFERENCE
 Align seg 1/1 to: AW090901
 Percent Similarity:
 JOURNAL
 TITLE
 ORGANISM
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 350
 320
 315
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 265
 72
 source
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 ACGTCAAGAGCACCATGGGGAAGCCATACAGG 409
 leIleSerPheLeuTrpValLysProTyrArg 99
 ·····AGCGTGAACTTCCTTGTTTCCCTTCTGAAG.....
 YHisThrAlaIleLeuAlaProAsnArgTrpGlnGluIleLeuSerLeuI 89
 ArgLeuThrIleSerAlaLeuLeuThrAlaLeuLeuValThrGlyCysVa 23
 gb_est2:BI675165
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 Quality:
 Tel: 650 723 2227 Fax: 650 725 8221
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 554)
 Department of Biological Sciences
Stanford University
 Email: walbot@stanford.edu
Plate: 614068 row: C col
 855 California Ave, Palo Alto,
 Contact: Walbot
 Unpublished (1999)
 University
 Maize ESTs from various cDNA libraries sequenced
 Walbot, V.
 Zea mays
 Zea
 Ratio:
 143
 mays
 Ø
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/dev_stage="3-4 days old"
/lab_host="XLOLR"
/note="form:
 75.50
1.606
50.000
 Lab
 /note="Organ: root; Vector: pBlueScriptII SK+; Site_1:
ECORI; Site_2: XhoI; 3-4 days old root tissue from Walbot
 Organism="Zea mays"
Cultivar="W23"
 Location/Qualifiers
 (LM)"
129 c
 from: 1
 AAGAACTGGCAGAATGTGAGATGCCTCT
 Gaps: 4
Percent Identity: 25.532
 142 g
 column:
 557
 .
6
 ď
 140 t
 80
 CA 94304,
 mRNA
 USA
 94
 linear
 377
 319
 264
 at Stanford
EST 12-SEP-2001
 alignment_block:
US-10-048-197-2 x BI675165/rev
 REFERENCE
AUTHORS
TITLE
 SOURCE
ORGANISM
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ORIGIN
 FEATURES
 COMMENT
 ACCESSION
VERSION
 Align seg 1/1 to reverse of: BI675165
 Percent Similarity:
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 JOURNAL
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 337 AAGGCAACCGTCAAATTCCAGCTCAAGAAGGTCCTTTGCATGGGC...GT 291
 39 luGlnThrIleIleLysGlyLysThrAsnLysGlnGluIleSerSerArg
 23 lSerThrGlyAsnValAlaMetLysGlu...GlnAsnGlnGlnThrIleG 39
 source
 7 ArgLeuThrIleSerAlaLeuLeuThrAlaLeuLeuValThrGlyCysVa
 Quality:
 Ratio:
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75.50 1.606 50.000

Gaps: Percent Identity:

Length:

94 4 25.532

from: 1

ţo:

55 236

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DEFINITION
 Zea mays.
Zea mays
 Unpublished (1999)
Contact: Walbot V
Department of Biological Sciences
 Plate: 949079 row: C
 R855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbotestanford.edu
 Stanford University
 University
 clade; Panicoideae;
1 (bases 1 to 557)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
 B1675165.1 GI:15590549
 Zea mays cDNA, mRNA sequence. BI675165
 949079C10.x2 949 - Juvenile leaf and shoot cDNA from Steve Moose
 Walbot, V
 Maize ESTs from various cDNA libraries sequenced
 143
/note="Organ: juvenile vegetative shoots; Vector:
pAD-GAL4-2.1; Site_1: EcoRI; Site_2: Nho1; Equal amounts
of total RNA by weight from 4 tissue sources (see below)
were pooled, polyA+ RNA isolated, and cDNA synthesized for
ECORI (5') and XhoI (3') directional cloning into lambda
Hybrizap vector from Stratagene. Tissue Sources: 1. Whole
shoots 3 days after sowing/imbibing in wet soil. 2. Basal
1.5 cm shoots 6 days after sowing - includes yellow
portions of developing leaves 1-5, primordia from 6-8, and
the vegetative apex. 3. Non-green portions of developing
leaves 4-5 and the vegetative apex, including adult leaf
primordia, 9 days after sowing. 4. Partially expanded and
greening leaves 4-5 at 13 days after sowing.*
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/db_xref="taxon:4577"
/clone_lib="949 - Juve
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meristem"
 /dev_stage="4 stages from 3-13 days after
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 Juvenile leaf and shoot cDNA from Steve
 10.
 at Stanford
 imbibing"
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BASE COUNT
ORIGIN
 REFERENCE
AUTHORS
 ACCESSION
VERSION
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US-10-048-197-2 x AI714378/rev
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LOCUS AI714378
 KEYWORDS
 DEFINITION
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 Ratio:
Percent Similarity:
 TITLE
 JOURNAL
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 205
 346
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68
 72
 56
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 ArgLeuThrIleSerAlaLeuLeuThrAlaLeuLeuValThrGlyCysVa
 ACGTCAAGAGCACCATGGGGAAGCCATACAGG
 PheGlySerAlaAspSerIleSerPheMetIleValValIleLysPheGl
 Zea mays.
Zea mays
 EST.
 Email: walbot@stanford.edu
Plate: 606013 row: A column:
Location/Qualifiers
 Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA
Tel: 650 723 2227
Fax: 650 725 8221
 Walbot, V
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.
 AI714378.1 GI:5018185
 mays cDNA, mRNA sequence.
AI714378
 606013A04.x2 606 - Ear tissue
 Contact: Walbot
 Unpublished (1999)
 University
 Maize ESTs from various cDNA libraries sequenced at Stanford
 (bases 1 to 559)
 144
 ø
 75.50
1.606
50.000
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; Site_2: XhoI; Mixed ear tissue cDNA library from Schmidt
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/cultivar="0hio43"
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 136 с
 AAGAACTGGCAGAATGTGAGATGCCTCT 178
 Percent
 Andropogoneae;
 126 g
 Gaps:
Identity:
 e cDNA
 from:
 146
 99
 CA 94304, USA
 04.
 153 t
 mRNA
. library
 Н
 25.532
 .
0
 94
 cDNA library from
 559
 from
 linear
 ar EST
 39
 297
 23
 lab
 Schmidt
 02-FEB-2000
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BASE COUNT
ORIGIN
 JOURNAL COMMENT
 SOURCE
ORGANISM
 REFERENCE
AUTHORS
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 seq_name:
 VERSION
 ACCESSION
 DEFINITION
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 Percent Similarity:
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 291
 9
 72
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.....AGCGTGAACTTCCTTGTTTCCCTTCTGAAG.....
 leIleSerPheLeuTrpValLysProTyrArg
 yHisThrAlaIleLeuAlaProAsnArgTrpGlnGluIleLeuSerLeuI 89
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 Quality:
Ratio:
 855 California Ave, Palo Alto,
Tel: 650 723 2227
Fax: 650 723 2221
Email: walbot@stanford.edu
Plate: 660069 row: A column:
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.
 Unpublished (1999)
Contact: Walbot V
 Walbot, V.
Maize ESTs from various cDNA libraries sequenced
 Zea mays
 mRNA sequence.
AW566286
 660069A03.y1 660 -
 Stanford University
 Department of Biological Sciences
 University
 zea mays.
 AW566286.1 GI:7227645
 (bases 1 to 563)
 146
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Directionally sequenced with 5'
Created by Amie Franklin."
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/db_xref="taxon:4577"
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1.606
50.000
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 Percent
 563 bp
stages
 ţ.
 Gaps:
Identity:
 Length:
 202
 99
 563
 03
 CA 94304,
 of.
 mRNA linear E
anther and pollen
 94
4
25.532
 Lambda Zap; Site_1: EcoRI; n cDNA library.
 USA
 end at the EcoRI site.
 262
 23
 at Stanford
 EST 10-MAR-2000
 mays
 shed"
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ORIGIN
 REFERENCE
AUTHORS
 VERSION
KEYWORDS
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 Ratio:
Percent Similarity:
 ACCESSION
 TITLE
 ORGANISM
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 426
 421
 371
 324
 484
 89
 56
 39
 23
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 PheGlySerAlaAspSerIleSerPheMetIleValValIleLysPheGl
 ACGTCAAGAGCACCATGGGGAAGCCATACAGG 515
 leIleSerPheLeuTrpValLysProTyrArg 99
 AGATG.....
 luGlnThrIleIleLysGlyLysThrAsnLysGlnGluIleSerSerArg 55
 lSerThrGlyAsnValAlaMetLysGlu...GlnAsnGlnGlnThrIleG 39
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 CDNA, mRNA sequence.
BF728138
BF728138.1 GI:12045908
EST.
 Stanford University
855 California Ave, Palo Alto,
 Quality:
 Email: walbot@stanford.edu
Plate: 1000056 row: E colu
Location/Qualifiers
 Unpublished (1999)
Contact: Walbot V
 Department of Biological Sciences
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
 Zea mays
 1000056E09.x2 1000 - Unigene
 University
 Maize ESTs from various cDNA libraries sequenced at Stanford
 Walbot, V
 clade; Panicoideae; Andropogoneae;
 Zea mays.
 (bases 1 to 587)
 157
 650 723 2227
650 725 8221
 75.50
1.606
50.000
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/db_xref="taxon:4577"
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 Gaps:
Percent Identity:
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I from Maize Genome Project Zea mays
 Length:
 CA
 9
 94304, USA
 Zea.
 94
4
25.532
 425
 420
 72
 EST 09-JAN-2001
 REFERENCE
AUTHORS
 SOURCE
ORGANISM
 FEATURES
 COMMENT
 KEYWORDS
 DEFINITION
 VERSION
 ACCESSION
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 US-10-048-197-2 x BF728138/rev
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BG842695
 On May 25,
 Zea mays
 Zea mays.
 BG842695.2
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 39 luGlnThrIleIleLysGlyLysThrAsnLysGlnGluIleSerSerArg
 23 lSerThrGlyAsnValAlaMetLysGlu...GlnAsnGlnGlnThrIleG
 PheGlySerAlaAspSerIleSerPheMetIleValValIleLysPheGl
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 AAGAACTGGCAGAATGTGAGATGCCTGT 226
 YH1sThrAlaIleLeuAlaProAsnArgTrpGlnGluIleLeuSerLeuI
 FORWARD: T7-1 (AA TAC GAC TCA CTA TAG)
BACKWARD: T3 (ATT AAC CCT CAC TAA AG)
Seg primer: primer T3 (ATT AAC CCT CAC
 G405 Agronomy, Iowa State University, Ames, Tel: 515-294-0975
 Contact: Patrick S. Schnable Schnable Laboratory
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.
 BG842695 599 bp mRNA linear E9 MEST39-A03.T3 ISUM4-TN Zea mays cDNA clone MEST39-A03
 PCR PRimers
 Fax: 515-294-2299
 Unpublished
 Qiu, F., Cui, F., Guo, L.,
 Email: schnable@iastate.edu
 Iowa State University
 Expressed Sequence Tags
 (bases 1 to 599)
 to reverse of: BF728138
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/cultivar="B73"
/db_xref="taxon:4577"
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/lab_host="DH10B"
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 (2001)
 Ashlock,D.A, Wen,T.J. and Schnable,P.S. from B73 Maize Seedlings and Silks
 from: 1
 99
 CCT CAC
 6
 TAA AG).
 587
 IA 50011-1010,
 g1:14209017
 89
 254
 72
 284
 55
 289
 39
 339
 23
 EST 29-MAY-2001
)3 3', mRNA
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AUTHORS
TITLE
 ACCESSION
VERSION
KEYWORDS
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 BASE COUNT
ORIGIN
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 SOURCE
 DEFINITION
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 Percent Similarity:
 ORGANISM
 JOURNAL
 309
 314
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 364 TGCCGTTGGCAACTTGGCGATGGAGGAGGAGCAGATCCAGCAGAACATCC
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 72
 56 PheGlySerAlaAspSerIleSerPheMetIleValValIleLysPheGl 72
 39 luGlnThrIleIleLysGlyLysThrAsnLysGlnGluIleSerSerArg
 23 lSerThrGlyAsnValAlaMetLysGlu...GlnAsnGlnGlnThrIleG
 7 ArgLeuThrIleSerAlaLeuLeuThrAlaLeuLeuValThrGlyCysVa
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 yHisThrAlaIleLeuAlaProAsnArgTrpGlnGluIleLeuSerLeuI
 gb_est1:AI691931
 Quality:
Ratio:
 Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
 Walbot, V.
Maize ESTs from various cDNA libraries sequenced at Stanford
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 602)
 Contact: Walbot V
 Unpublished (1999)
 Zea mays
 Zea mays.
 AI691931.1 GI:4966852
 mays cDNA, mRNA sequence.
 606007A02.x1 606 - Ear tissue
Email: walbot@stanford.edu
Plate: 606007 row: A col
 160
 as a template for DNA PolI-catalyzed second strand synthesis. After the addition of EcoRI adaptors, the ds-cDNAs were digested with NotI and size-selected. The resulting molecules were directionally cloned into the EcoRI and NotI sites of the pT7T3PAC vector. The library then went through one round of normalization to CoT value of 5 based on the methods of Marcelo Bento Soares (Genome Research 6: 791-805, 1996)."
 75.50
1.606
50.000
 AAGAACTGGCAGAATGTGAGATGCCTCT 252
 Length:
Gaps:
Percent Identity:
column:
 bp mRNA
cDNA library
 from: 1
2
 94
4
25.532
 .
6
 from
 linear
 ar EST 02-FEB-2000
Schmidt lab Zea
 89
 310
 55
 315
 39
 365
 23
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REFERENCE
AUTHORS
TITLE
 SOURCE
ORGANISM
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US-10-048-197-2 x AI691931/rev
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 COMMENT
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 ACCESSION
 DEFINITION
 BASE COUNT
 Align seg 1/1 to reverse of: AI691931
 Percent Similarity:
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 312
 317
 254
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 source
 9
 72
 56
 39
 23 | SerThrGlyAsnValAlaMetLysGlu...GlnAsnGlnGlnThrIleG
 7 ArgLeuThrIleSerAlaLeuLeuThrAlaLeuLeuValThrGlyCysVa
 ACGTCAAGAGCACCATGGGGAAGCCATACAGG
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 AAGAACTGGCÄĞAATGTGAGATGCCTCT
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 PheGlySerAlaAspSerIleSerPheMetIleValValIleLysPheGl 72
 AGATG.....
 luGlnThrIleIleLysGlyLysThrAsnLysGlnGluIleSerSerArg
 Qiu,F., Cui,F., Guo,L., A
Expressed Sequence Tags f
Unpublished (2001)
Contact: Patrick S. Schna
Schnable Laboratory
 2ea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Trache
Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae;
clade; Panicoideae; Andropogoneae; Zea.
 sequence.
BM079588
 BM079588 607 bp mRNA linear EST 14-NOV-2001 MEST96-F07.T3 ISUM4-TN Zea mays cDNA clone MEST96-F07 3', mRNA
 EST
 Quality:
 BM079588.1
 Zea mays.
 Ratio:
 (bases 1 to 607)
 151
 State University
 Agronomy,
 D)
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/cultlvar="ohio43"
/db_xref="taxon:4577"
/clone_lib="606 - Ear 1
lab"
 lab"
 Patrick S. Schnable
 75.50
1.606
50.000
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/dev_stage="ear length from 0.5 cm - 2.0 cm"
/dev_stage="ear length from 0.5 cm - 2.0 cm"
/lab_host="XIOLR (Stratagene)"
/note="Organ: immature ear; Vector: pBK-CMV; Site_1:
/note="Organ: immature ear; Vector: pBK-CMV; Site_1:
 Location/Qualifiers
 Site_2: XhoI; Mixed ear tissue cDNA
 GI:16926520
 AGCGTGAACTTCCTTGTTTCCCTTCTGAAG.....
 144 c
Iowa State University,
 Length:
Gaps:
Percent Identity:
 133 g
 Ashlock,D.A, Wen,T.J. and from B73 Maize Seedlings &
 Ear tissue cDNA library from Schmidt
 from: 1
 99
 174 t
 25
 Ames,
 8
 .532
 IA 50011-1010, USA
 library
 283
 313
 55
 318
 39
 368
 Schnable, P.S. and Silks
 Tracheophyta;
aceae; PACC
 from
 1: EcoRI
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US-10-048-197-2 x BM079588/rev
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 BASE COUNT
 FEATURES
 Align seg 1/1 to reverse of: BM079588
 Percent Similarity:
 315
 370
 417 AAGGCAACCGTCAAGTTCCAGCTCAAGAAGGTTCTTTGCATGGGT...GT 371
 source
72 yHisThrAlaIleLeuAlaProAsnArgTrpGlnGluIleLeuSerLeuI 89
 56
 39 luGlnThrIleIleLysGlyLysThrAsnLysGlnGluIleSerSerArg 55
 23 1SerThrGlyAsnValAlaMetLysGlu...GlnAsnGlnGlnThrIleG 39
 7 ArgLeuThrIleSerAlaLeuLeuThrAlaLeuLeuValThrGlyCysVa 23
 AGCGTCAACTTCCTTGTTTCCCTTCTGAAG.....
 PheGlySerAlaAspSerIleSerPheMetIleValValIleLysPheGl 72
 TGCCGTTGGCAACTTGGCGATGGAGGAGAAGCAGATCCAGCAGAACATCC
 rt). Overall sequence quality assessment and vector trimming were conducted using the Lucy software (http://www.tigr.org/softlab/). Lucy parameters were set to ensure the consent of the chosen better without any vector fragments in the chosen high-quality region of each sequence. Low-quality bases between the poly-T and the high-quality region were replaced with N's to serve
 Quality:
 Email: schnable@iastate.edu
Individual basecall and confidence value were assigned using
 BACKWARD: Backward PCR primer sequence, primer T3
 FORWARD: Forward PCR primer sequence, primer T7-1 (AA TAC GAC TCA
 (<http://depts.washington.edu/ventures/collabtr/direct/index.htm>#b
 Phred software,
 spacers.
 primer: primer T3 (ATT AAC CCT CAC TAA AG).
 158
 PRimers
 resulting molecules were directionally cloned into the BCORI and NotI sites of the pT7T3PAC vector. The library then went through one round of normalization to CoT value of 5 based on the methods of Marcelo Bento Soares (Genome Research 6: 791-806, 1996).*

144 c 128 g 177 t
 as a template for DNA PolI-catalyzed second strand synthesis. After the addition of EcoRI adaptors, the ds-cDNAs were digested with NotI and size-selected.
 75.50
1.606
50.000
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/clone="MEST96-F07"
 /organism="Zea mays"
/cultivar="B73"
 /tissue_type="Seedling and silk"
/lab_host="DH10B"
 /clone_lib="ISUM4-TN"
 tion/Qualifiers
 Percent Identity:
 from: 1 to:
 94
4
25.532
 (ATT AAC
 CCT CAC
 the
 the
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REFERENCE
AUTHORS
 ACCESSION
VERSION
 seq_documentation_block:
LOCUS AW324655
 alignment_block:
 COMMENT
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 FEATURES
 SOURCE
 BASE COUNT
 KEYWORDS
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 Percent Similarity:
 JOURNAL
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 ORGANISM
 341
 388 AAGGCAACAGTCAAGTTCCAGCTCAAGAAGGTCCTTTGCATGGGT...GT 342
 source
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 89
39
 23
 7 ArgLeuThrIleSerAlaLeuLeuThrAlaLeuLeuValThrGlyCysVa
 lSerThrGlyAsnValAlaMetLysGlu...GlnAsnGlnGlnThrIleG
|::::::||||||:::||| ||| ||| ||||:::|||:
luGlnThrIleIleLysGlyLysThrAsnLysGlnGluIleSerSerArg
 ACGTCAAGAGCACCATGGGGAAGCCATACAGG 226
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 Quality:
Ratio:
 Zea mays.
Zea mays
 Email: walbot@stanford.edu
Plate: 707036 row: H column:
 855 California Ave, Palo Alto,
Tel: 650 723 2227
Fax: 650 725 8221
 Stanford University
 Contact: Walbot V
Department of Biological Sciences
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
 EST.
 mays cDNA, mRNA sequence.
 707036H01.x1 707 - Mixed adult
 Unpublished (1999)
 Walbot, V.
 AW324655.1 GI:6760556
 University
 Maize ESTs from various
 clade; Panicoideae;
 (bases 1 to 611)
 155
 Ø
 /note="Organ: tassel, kernel, silk, husk, root, leaf; vector: pGADIO; Site_1: EcoRI; cDNA library from fully differentiated maize tissues from an active Mutator plant. Tissue ratio is 4/2/1/1/1/1 (tassel, kernel, silk, husk, root, leaf). Unidirectionally cloned."

153 c 133 g 170 t
 75.50
1.606
50.000
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/dev_stage="adult"
/lab_host="DH10B"
 /cultivar="W23"
/db_xref="taxon:4577"
/clone_lib="707 - Mixo
 Location/Qualifiers
 organism="Zea mays"
 Length:
Gaps:
Percent Identity:
 Andropogoneae;
 cDNA libraries sequenced
 611 bp
 Mixed adult tissues from Walbot lab
 from: 1
 01
 CA 94304, USA
 tissues from Walbot lab (SK) Zea
 mRNA
 94
4
25.532
 .
5
 611
 linear
 55
 39
 23
 at Stanford
 root, leaf"
 EST 27-JAN-2000
 (SK
```

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JOURNAL COMMENT
 REFERENCE
AUTHORS
 SOURCE
ORGANISM
 ACCESSION
VERSION
KEYWORDS
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US-10-048-197-2 x AI711637/rev
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tocus AI711637
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 BASE COUNT
ORIGIN
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 DEFINITION
 Align seg 1/1
 Ratio:
Percent Similarity:
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 source
 286
 228 ACGTCAAGAGCACCATGGGGAAGCCATACAGG 197
 291
 89
 72
23 lSerThrGlyAsnValAlaMetLysGlu...GlnAsnGlnGlnThrIleG
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 ArgLeuThrIleSerAlaLeuLeuThrAlaLeuLeuValThrGlyCysVa 23
 AAGAACTGGCAGAATGTGAGATGCCTGT 229
 AGATG.....
 yHisThrAlaIleLeuAlaProAsnArgTrpGlnGluIleLeuSerLeuI 89
 PheGlySerAlaAspSerIleSerPheMetIleValValIleLysPheGl 72
 Zea mays.
Zea mays
 Quality:
 Unpublished (1999)
Contact: Walbot V
 AI711637 605 - Endosperm
 Email: walbot@stanford.edu
Plate: 605058 row: E column:
 Stanford University
 Department of Biological Sciences
 Walbot, V.
 clade; Panicoideae; Andropogoneae; Zea.
l (bases 1 to 613)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
 AI711637.1 GI:5005575
 Maize ESTs from various cDNA libraries sequenced at Stanford
 cDNA, mRNA sequence.
 to reverse of: AI711637
 California Ave, Palo Alto,
 158
 650 723 2227
650 725 8221
 ø
 lab"
 /organism="Zea mays"
/cultivar="Ohio43"
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/db_xref="taxon:4577"
/clone_lib="605 - Endosperm cDNA library from Schmidt lab"
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/dev_stage="10-14 days post-pollination"
/dev_stage="10-14 days post-pollination"
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/lab_host="DH5(alpha)"
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Site_2: XhoI; Kernel endosperm cDNA library from Schmidt
 75.50
1.606
50.000
 Location/Qualifiers
 AGCGTCAACTTCCTTGTTTCCCTTCTGAAG....
 158 c
 Percent
 :
 138
 g
 Gaps:
Identity:
 cona
 from:
 06
 CA 94304,
 159 t
 mRNA
11brary
 _
 94
4
25.532
 to: 613
 from
 rom Schmidt
 39
 257
 02-FEB-2000
 Zea
 mays
```

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REFERENCE
AUTHORS
 VERSION
KEYWORDS
SOURCE
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 Quality:
 BASE COUNT
ORIGIN
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Percent Similarity:
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 265
 315
 202
 89
 72
 56
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 luGlnThrIleIleLysGlyLysThrAsnLysGlnGluIleSerSerArg 55
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 lelleSerPheLeuTrpValLysProTyrArg
 AGCGTGAACTTCCTTGTTTCCCTTCTGAAG.....
 gb_est1:AW927882
 Zea mays
Eukaryota; Viridiplantae; Streptophyta; Em
Spermatophyta; Magnollophyta; Lillopsida;
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 614)
 855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
 AW927882.1 GI:8103229
EST.
 945010D06.Y1 945 - Mixed (SK) Zea mays cDNA, mRNA
 Plate: 945010 row: D column: 06.
Location/Qualifiers
 Department of Biological Stanford University
 Contact: Walbot
 Unpublished (1999)
 Walbot,V.
Maize ESTs from various cDNA libraries sequenced
 AW927882
 174
 /note="Organ: tassel, kernal, silk, husk, root, leaf;
Vector: pGAD10; Site_1: ECORI; cDNA library from fully
differentiated maize tissues from an active Mutator plant.
Tissue ratio is 4:2:1:1:1:1 (tassel, kernel, silk, husk,
root, leaf). Unidirectionally cloned. New library number
given to library 707 for additional sequencing."
a 133 c 149 g 158 t
75.50
1.606
50.000
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same as 707 (SK)"
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 /organism="Zea mays"
/cultivar="W23"
Gaps:
Percent Identity:
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 614 bp mRNA
d adult tissues :
A sequence.
 Sciences
 171
 99
 mRNA
25.532
 from
 Embryophyta; Tracheophyta;
a; Poales; Poaceae; PACC
 494
 linear EST
n Walbot lab,
 from
 231
 261
 at
 Walbot lab,
 Stanford
 same
 30-MAY-2000
same as 707
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alignment\_block: US-10-048-197-2

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AW927882

1/1

. 6

AW927882

from: 1

ç O:

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BASE COUNT
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 COMMENT
 Percent Similarity:
 REFERENCE
 SOURCE
 VERSION
 ACCESSION
 DEFINITION
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 Align seg
 AUTHORS
TITLE
 ORGANISM
 JOURNAL
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 247
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 23
 7 ArgLeuThrIleSerAlaLeuLeuThrAlaLeuLeuValThrGlyCysVa
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 Quality:
 Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA
 Unpublished (1999)
Contact: Walbot V
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.
 Tel: 650 723 2227 Fax: 650 725 8221
 Walbot, V.
Maize ESTs from various
 AI820102
AI820102.1 GI:5439181
 Plate:
 Zea mays
 cDNA, mRNA sequence.
 605086A01.x3 605 -
 Ratio:
 (bases 1 to 624)
 161
 walbot@stanford.edu
605086 row: A colu
 Ø
 75.50
1.606
50.000
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/db_xref="taxon:4577"
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/lab_host="DH5(alpha)"
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/cultivar="Ohio43"
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 162 c
Length:
Gaps:
Percent Identity:
 Endosperm
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 139
 cDNA libraries sequenced
 g
 624
 bp mRNA
cDNA library
 391
 ဌ
 160 t
 94304,
 94
4
25.532
 2 others
 from
 linear EST 02-FEB-2000 from Schmidt lab Zea mays
 55
 39
 246
 23
 301
 at Stanford
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JOURNAL
COMMENT
 REFERENCE
AUTHORS
TITLE
 FEATURES
 SOURCE
ORGANISM
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US-10-048-197-2 x AI820102/rev
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 Align seg 1/1 to reverse of: AI820102
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 259
 264 AGATG.....
 361 AAGGCAACCGTCAAGTTCCAGCTCAAGAAGGTCCTTTGCATGGGC...GT 315
 201 ACGTCAAGAGCACCATGGGGAAGCCATACAGG 170
 68
 56
 72
 39 luGlnThrIleIleLysGlyLysThrAsnLysGlnGluIleSerSerArg 55
 23 | SerThrGlyAsnValAlaMetLysGlu...GlnAsnGlnGlnThrIleG
 7 ArgLeuThrIleSerAlaLeuLeuThrAlaLeuLeuValThrGlyCysVa
 leIleSerPheLeuTrpValLysProTyrArg 99
 AAGAACTGGCAGAATGTGAGATGCCTCT 202
 yHisThrAlaIleLeuAlaProAsnArgTrpGlnGluIleLeuSerLeuI 89
 PheGlySerAlaAspSerIleSerPheMetIleValValIleLysPheGl 72
 Zea mays.
Zea mays
 855 California Ave, Palo Alto, Tel: 650 723 2227 Fax: 650 725 8221
 Department of Biological Sciences Stanford University
 Unpublished (1999)
Contact: Walbot V
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 634)
 946020H06.x1 946 - tassel
 Walbot, V.
Maize ESTs from various
 EST.
 mays cDNA, mRNA sequence.
 University
 BE509707.1 GI:9730955
 walbot@stanford.edu
946020 row: H colum
Location/Qualifiers
/note="Organ: tassels; Vector: HybriZAP; Site_1: EcoRI; Site_2: XhoI; George Chuck dissected immature tassels between 1mm and 3mm. Sharon Stanfield prepared the cDI Library in HybriZAP. Sample insert size range was 350 to 3 Kb with a 1 Kb average."
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inflorescence development"
/lab_host="XLOLR"
 /organism="Zea mays"
/cultivar="OH43"
/db_xref="taxon:4577"
/clone_lib="946 – tassel primordium
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 AGCGTGAACTTCCTTGTTTCCCTTCTGAAG
 cDNA libraries
 634 bp
 primordium
 from: 1
 CA
 90
 94304, USA
 mRNA
 prepared
 ç
O:
 sequenced
 linear
red by S
 prepared
 230
 260
 39
 23
 at
 Schmidt lab
 Stanford
 EST 07-AUG-2000
 by Schmidt
```

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BASE COUNT
ORIGIN
 REFERENCE
AUTHORS
TITLE
 SOURCE
ORGANISM
 alignment_block:
US-10-048-197-2 x BE509707/rev
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 COMMENT
 seq_documentation_block:
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 VERSION
 ACCESSION
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Zea mays
 Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA
Tel: 650 723 227
Fax: 650 725 8221
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 Unpublished (1999)
On May 11, 1999 this sequence version Contact: Walbot V
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Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
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 ATTORNEY/AGENT INFORMATION:
NAME: Ralph, Rebecca L.
REGISTRATION NUMBER: 35,152
REFERENCE/DOCKET NUMBER: CH
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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 APPLICANT: Weiser, Jeffrey M.
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Percent Similarity:
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APPLICANT: Weinstein, Jasminder
TITLE OF INVENTION: No. 6291642el Mammalian Cell Cycle Protein
FILE REFERENCE: 06843.0026-04; A-283 D
CURRENT APPLICATION NUMBER: US//8/988,856B
CURRENT FILING DATE: 1997-12-11
NUMBER OF SEQ ID NOS: 31
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 19 ValThrGlyCysValSerThrGlyAsnValAlaMetLysGluGlnAsnGl 35
 GCGCGGATCTGGCCAGAAGTGAATGCACCAACATCCATAACTCCTCGG 426
 AsnArgTrpGlnGluIleLeuSerLeuIleIleSerPheLeuTrp 94
 67.50
1.298
52.000
 66.50
1.583
65.625
 Percent Identity: 28.000
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 from: 1
 from: 1
 to: 1700
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 612
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US-10-048-197-2 x PCT-US95-01806-3/rev
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 Percent Similarity:
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 1131
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 1181 TTGATGCTGGGTGAATGTCTGCAGAGGAACCCAGCCACCCTCTCCAGGAG 1132
 1040
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
 1090 GCCAAATGTCGTCCATCTGGGGCCCAGCGCCACACACACTTCCTGGCT 1041
 1181 TTGATGCTGGGTGAATGTCTGCAGAGGAACCCAGCCACCCTCTCCAGGAG
.090 GCCAAATGTCGTCCATCTGGGGCCCAGCGCAGCCCACACACTTCCTGGCT 1041
 STREET: 1840 CITY: Thousand Oaks
STATE: California
 FEATURE:
 NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
 APPLICANT: Weinstein, Jasminder TITLE OF INVENTION: Novel Mamma
 MOLECULE TYPE:
 50 lnGluIleSerSerArgPheGlySerAlaAspSerIleSerPheMetIle 66
 17
 50 lnGluIleSerSerArgPheGlySerAlaAspSerIleSerPheMetIle 66
 33 nAsnGlnGlnThrIleGluGlnThrIleIleLysGlyLysThrAsnLysG 50
 TYPE: nucleic acid
STRANDEDNESS: unknown
 CLASSIFICATION:
 APPLICATION NUMBER: FILING DATE:
 NAME/KEY:
 TOPOLOGY:
 LOCATION:
 ADDRESSEE:
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 91320-1789
 Ratio:
 E: Amgen Inc./Patent Operations/RBW 1840 Dehavilland Drive
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117..1616
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 66.50
1.583
65.625
 Novel Mammalian Cell Cycle Protein
 PCT/US95/01806
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Rd Genome

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 ; TYPE: DNA
; ORGANISM: Glycine
US-09-196-520-5
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 Percent Similarity:
 GENERAL INFORMATION:
APPLICANT: Falco, Carl S.
APPLICANT: Allen, Stephen M.
TITLE OF INVENTION: plant Isocitrate Dehydrogenase Homologs
FILE REFERENCE: BB-1291
 Sequence 333, Application PC/TUS9605320A GENERAL INFORMATION:
 SOFTWARE:
SEQ ID NO 5
 Sequence 5, Application US/09196520 Patent No. 6204039
 CURRENT FILING DATE: 1998-11-19
EARLIER FILING DATE: December: 60/067,388
EARLIER FILING DATE: December 2, 1997
NUMBER OF SEQ ID NOS: 10
 CURRENT APPLICATION NUMBER: US/09/196,520
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 1043 TGACAAAGCAGAACAGATTCAAAAAAGCCATCCTGAACACAATTGCAGAAG 1092
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 102
 APPLICANT:
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 APPLICANT:
 993 ACTGCTTTACTGCTAAGTGGTGTTACAATGTTGCGCCATTTGAACCTCCA 1042
 45
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 ValValIleLysPheGlyHisThrAlaIleLeuAlaProAsn
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 LysGluGlnAsnGlnGlnThrIleGluGlnThrIleIleLysG 45
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 Quality:
 PatentIn Ver. 2.0
 Ratio:
Human Genome Sciences
9410 Key West Avenue
Rockville, MD 20850
 1.100
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 Percent
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 26.606
 999
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Percent Similarity:
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 TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 402 base pairs
 APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT:
 APPLICANT:
 REGISTRATION NUMBER: 36,688
REGISTRATION NUMBER: 144
REFERENCE/DOCKET NUMBER: 144
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
 APPLICATION NUMBER: 08/487,429
FILING DATE: June 7, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Erick Steffe
 APPLICATION NUMBER: 08/47/
FILING DATE: June 7, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/48
 CLASSIFICATION:
PRIOR APPLICATION DATA:
 SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PC:
FILING DATE: April22,
 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
 APPLICANT: J. Craig Venter
TITLE OF INVENTION: Nucleotide Sequence of the Haemophilus Influenzae
NUMBER OF SEQUENCES: 48
 CORRESPONDENCE ADDRESS
 .11
 APPLICANT:
 41 hrIleIleLysGlyLysThrAsnLys 49
 27 nValAlaMetLysGluGlnAsnGlnGlnThrIleGlu......GlnT 41
 16
 COMPUTER: HP Vect
OPERATING SYSTEM:
 STREET: 1100 New CITY: Washington
 STATE: D.C
 ADDRESSEE:
 SerAlaLeuLeuThrAlaLeuLeuValThrGlyCysValSerThrGlyAs 27
 TCTCTTATTTTACCGCACTTTTAATGACTGGCTGTGCCAAAATGCGAA 65
 CCTTACAAAAAGGCGAAGCTGNTCGA 141
 TGTAACAACACCTCAAGCGCAAAAAATGCAAGTAGAAAAAGTGGATAAAG
 Quality:
 20003-3934
 nucleic acid
 E: Sterne, Kessler, G
1100 New York Avenue,
 USA
 Mark D. Adams
 United States of America
Johns Hopkins University
 Hamilton O. Smith
 United States of America
 Baltimore, MD 21205
 E: Diskette, 3
 720 Rutland Avenue
 linear
 April22, 1996
 65.50
2.047
76.190
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 371-2540
 MSDOS version 6.2
 08/476,102
 PCT/US96/05320A
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 3.50 inch, 1.4Mb storage
 1488.014PC01
 Goldstein & Fox
e, Suite 600
 ç
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Quality:
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US-10-048-197-2 x US-08-371-377-16
 seq_documentation_block:
 US-08-371-377-16
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 Ratio:
Percent Similarity:
 Patent No.
 Sequence 16,
 ATTORNEY AGENT INFORMATION:

NAME: White, John P.

REGISTRATION NUMBER: 28,678

REFERENCE/DOCKET NUMBER: 0575

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 278-0400
 TELEFAX: (212) 391-05
INFORMATION FOR SEQ ID NO:
 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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 TOPOLUGE
MOLECULE TYPE: CD
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LENGTH: 2128 base pairs
TYPE: nucleic acid
 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
 696 ATTGATGCCCCAGGACACAGAGACTTTATCCAAAACATGATTACAGGGAC 745
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796 TTGAAGCTGGTATCTCCAAGAATGGGCAGACCCGACAGCATGCCCTTCTG 845
 FEATURE:
 ANTI-SENSE:
 TITLE OF INVENTION:
 APPLICANT:
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 49 LysGlnGluIleSerSerArgPheGlySerAlaAspSerIleSerPheMe 65
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 FILING DATE:
 APPLICATION NUMBER:
 COUNTRY:
 CLASSIFICATION: 435
 STREET:
 ADDRESSEE:
 10036
 6, Application US/08371377
5851764
 New York
 New York
 1185 Avenue of the Americas
 United States
 Fisher, Paul B.
Shen, Ruogian
 CDS
621..1817
 ĕ
 linear
 CDNA
 single
 64.50
1.057
51.261
 DEVELOPMENT OF DNA PROBES AND
IMMUNOLOGICAL REAGENTS SPECIFIC FOR CELL SURFACE-EXPRESSED
MOLECULES AND TRANSFORMATION-ASSOCIATED GENES
 US/08/371,377
 16:
 Percent Identity:
 of America
 0575/37590-B
 from: 1
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22.689
 2128
 695
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 seq_documentation_block:
 Ratio:
Percent Similarity:
 Sequence 2, Application US/07895300A Patent No. 5279823
 GENERAL INFORMATION: APPLICANT: Frenz,
 TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
 COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
SOFTWARE: Patin (Genentech)
 APPLICANT: Frenz, John
APPLICANT: Shire, Steven J.
APPLICANT: Sliwkowski, Mary B.
TITLE OF INVENTION: PURIFIED FORMS OF DNase
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
 APPLICATION NUMBER: UFILING DATE: 19920608 CLASSIFICATION: 424 PRIOR APPLICATION DATA:
 996
 SEQUENCE CHARACTERISTICS:
LENGTH: 1039 bases
 REFERENCE/DOCKET NUMBER: 74
TELECOMMUNICATION INFORMATION:
 ATTORNEY/AGENT INFORMATION: NAME: Hensley, Max D.
 SOFTWARE: patin (Genen CURRENT APPLICATION DATA:
 846 GCTTACACACTGGGTGTGAAACAACTAATTGTCGGTGTTAACAAAATGGA 895
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 88 euIleIleSerPheLeuTrpValLysProTyrArgProLysAsnLeuSer 104
 72 GlyHisThrAlaIleLeuAlaPro.AsnArgTrpGlnGluIleLeuSerL 88
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 TELEPHONE: 415/952-9881
TELEFAX: 415/952-9881
TELEX: 910/371-7168
TELEX: 910/371-710
 APPLICATION NUMBER: FILING DATE:
 COUNTRY: UZIP: 94080
 REGISTRATION NUMBER:
 ADDRESSEE:
 TTT 998
 tIle.....valValIleLysPhe.
 Quality:
 South San Francisco
 /AGENT 1...
Hensley, Max D.
Hensley, Max D.
27,043
 NUCLEIC ACID
 California
 E: Genentech, Inc.
460 Point San Bruno Blvd
 USA
 linear
 415/225-1994
 Genentech,
 19920608
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to: 1039

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 Sequence 2, Application US/08458367 Patent No. 5783433
 GENERAL INFORMATION:
APPLICANT: Frenz, John
APPLICANT: Shire, Steven J.
APPLICANT: Sliwkowski, Mary B.
APPLICANT: Sliwkowski, Mary B.
 FILING DATE: 02-Sep-
PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/348284
FILING DATE: 30 No. 5/83433-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/116186
 APPLICATION NUMBER: 08/409631 FILING DATE: 22-mar-1995 PRIOR APPLICATION DATA:
 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WinPatin (Genentech) CURRENT APPLICATION DATA:
 COMPUTER READABLE FORM: MEDIUM TYPE: 3.5 inc
 331
 295
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 195
 PRIOR APPLICATION DATA:
 430
 CORRESPONDENCE ADDRESS
 TITLE OF INVENTION: PURIFIED FORMS NUMBER OF SEQUENCES: 18
 64
 51
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 APPLICATION NUMBER: US/08/458,367
FILING DATE: 02-Jun-1995
 CITY: South San Francisco
STATE: California
 APPLICATION NUMBER: 07/895300
 CLASSIFICATION:
 COUNTRY:
 STREET:
 ADDRESSEE:
 GluIleSerSerArgPheGlySerAlaAspSerIleSerPh 64
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 94080
 E: Genentech, Inc.
460 Point San Bruno Blvd
 USA
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 02-Sep-1993
08-Jun-1992
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 OF DNase
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 TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
 CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
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 TITLE OF INVENTION: PURIFIED FORMS OF DNase NUMBER OF SEQUENCES: 17
 APPLICANT: Genentech,
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LENGTH: 1039 base pairs
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TELEPHONE: 415/25-3562
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STRANDEDNESS: Single
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Ratio:
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0.977
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 Inc.
 35,910
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 19
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 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 1039 bases
 APPLICATION NUMBER: POFILING DATE: 19930528
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
 NAME: Johnston, Sean A.
REGISTRATION NUMBER: P35,910
REFERENCE/DOCKET NUMBER: 7471
TELECOMMUNICATION INFORMATION:
 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: patin (Genentech) CURRENT APPLICATION DATA:
 ATTORNEY/AGENT INFORMATION:
 475
 380
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MEDIUM TYPE: 5.25 inch,
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 34 snGlnGlnThrIleGluGlnThrIleIleLysGlyLysThrAsnLysGln 50
 19 lThrGlyCysValSerThrGlyAsnValAlaMetLys.....GluGlnA 34
 3 AsnHisHisIleArgLeuThrIleSerAlaLeuLeuThrAlaLeuLeuVa 19
 TELEFAX: 415/77168
TELEX: 910/371-7168
 STRANDEDNESS:
 TELEPHONE:
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 oTyrArgProLysAsnLeuSer 104
 .TACAGGCCTGACCAGGTGTCT 495
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 Ratio:
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 63.50
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 to: 1039
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REFERENCE/DOCKET NUMBER: 792C:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-3567
TELEPAY:
 TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
 COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch,
COMPUTER: IBM PC compati
 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS SOTWARE: patin (Genentech) CURRENT APPLICATION DATA:
 FILING DATE:
ATTORNEY/AGENT INFORMATION:
 SEQUENCE CHARACTERISTICS:
LENGTH: 1039 bases
 CLASSIFICATION:
PRIOR APPLICATION DATA:
 CORRESPONDENCE ADDRESS:
 NUMBER OF SEQUENCES:
 TITLE OF INVENTION: Compaction Assay for Assessment of Respiratory Disease TITLE OF INVENTION: Therapy
 APPLICANT:
331 .CTGGTCCAGGAGGTCAGAGACAGCCACCTGACTGCCGTGGGGAAGCTGC 379
 295 TACATTGTGCAGATCCTGAGCCGCTATGACATCGCC........
 245 ACATCCAGACATTTGGGGAGACCAAGATGTCCAATGCCACCCTCGTCAGC
 51
 34 snGlnGlnThrIleGluGlnThrIleIleLysGlyLysThrAsnLysGln 50
 ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
 TYPE: nucleic acid
 APPLICATION NUMBER:
 APPLICATION NUMBER: FILING DATE:
 COUNTRY:
 STATE:
 STRANDEDNESS:
 GluIleSerSerArgPheGlySerAlaAspSerIleSerPh 64
 Quality:
 94080
 Ratio:
 California
 USA
 Genentech,
 linear
 63.50
0.977
52.419
 single
 PC-DOS/MS-DOS
 Inc.
 PCT/US93/10519
 Gaps:
Percent Identity:
 360 Kb floppy disk
 792C1
 Length:
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 294
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 Patent No. 6197551
 seq_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-013-810-1
 Align seg 1/1 to:
 ATTORNEY/AGENT INFORMATION:

NAME: Amy E. Mandragouras

REGISTRATION NUMBER: 36,207

REFERENCE/DOCKET NUMBER: MEI-010

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617)227-7400

TELEPAX: (617)742-4214

INFORMATION FOR SEO ID NO: 1:

SEQUENCE CHARACTERISTICS:
LENGTH: 746 base pairs
 Percent Similarity:
 GENERAL INFORMATION: APPLICANT: Busfie
4 HisHisIleArgLeuThrIleSerAlaLeuLeuThrAlaLeuLeuValTh 20
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117 CATCACCTTCGCTTAGACATGTTCAGGATCTTA......GTAGTCGTGTG 160
 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
 FEATURE:
 PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
 MOLECULE TYPE: cDNA
 APPLICANT: Busfield, Samantha J.
TITLE OF INVENTION: No. 6197551el TANGO 80 Molecules and Uses Thereof
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 CORRESPONDENCE ADDRESS:
 475
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 97
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 NAME/KEY:
 TOPOLOGY:
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 APPLICATION NUMBER: FILING DATE:
 CITY: Boston STATE: Massa
 CLASSIFICATION:
 COUNTRY:
 STREET:
 ADDRESSEE:
 TGGACAACCTCAATCAGGATGCACCAGACACCTATCACTACGTGGTCAGT 429
 .TACAGGCCTGACCAGGTGTCT 495
 oTyrArgProLysAsnLeuSer 104
 02109
 nucleic acid
 Ratio:
 Massachusetts
 3: LAHIVE & COCKFIELD, LLP
28 State Street
 CDS
135..428
 USA
 linear
 US-09-013-810-1
 single
 1.050
54.054
 63.00
 US/09/013,810
 Gaps:
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 from:
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 24.324
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; TYPE: DNA
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US-09-058-489-34
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 US-10-048-197-2 x US-09-058-489-34
 Percent Similarity:
 SOFTWARE: F
SEQ ID NO 34
 GENERAL INFORMATION:
APPLICANT: Whitehead Institute for Biomedical Research
 Sequence 34, Application US/09058489 Patent No. 6103886
 APPLICANT: Lahn, Bruce
APPLICANT: Page, David
TITLE OF INVENTION: Genes in the No. 6103886-Recombining Region
TITLE OF INVENTION: Chromosome
TILE REFERENCE: WHI97-08pA
CURRENT APPLICATION NUMBER: US/09/058,489
CURRENT FILING DATE: 1998-04-10
CURRENT FILING DATE: 1998-04-10
CARLIER FILING DATE: 1997-04-11
NUMBER OF SEQ ID NOS: 91
5482 CCAATGGA...AGCAATAAGCTGGAGGTGGAAGATGAACAAGTTTGCTGT 5528
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 411 GAGATGATTGTGGTACATTAAGGTTTTTAGA 441
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 361 GCCCACTCATTCTGACCCAAGAACTGGGGGAAATCTTCATCACTGACTTC 410
 161 TGGATCCTGCAGACAATATCCTCACTGCAGTCCCAAGGAAAGAGCAAAC 210
 10 IleSerAlaLeuLeuThrAlaLeuLeuValThrGlyCysValSerThrGl
 261 AAAGCCTCTCTTCTATCACAAGAAGAGTGGTACAACCTCTACATTTGA 310
 26 yAsnValAlaMetLysGluGlnAsnGlnGlnThrIleGluGlnThrIleI 43
 90 eSerPheLeuTrp...ValLysProTyrArg
 74 hrAlaIleLeuAla.ProAsnArgTrpGlnGluIleLeuSerLeuIleIl 90
 36
 57 ySerAlaAspSerIleSerPheMetIleValValIleLysPheGlyHisT 74
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 leLysGlyLysThrAsnLysGlnGluIleSerSerArgPheGlySerAla 59
 SerSerArgPheGl 57
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 1.086
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 Percent Identity: 23.301
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STRANDEDNESS:
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 Align seg 1/1 to: US-08-366-783-3
 Ratio:
Percent Similarity:
 TELEFAX: 415-324-0960
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 765 base pairs
TYPE: nucleic acid
 Patent No.
 APPLICANT: Molone
 equence 3, Application US/08366783 atent No. 5650554
 5640 CCAAGCA 5646
 5561 TTTACTTCCAACAGCGTTGGATGCACTTAGTAAAG....
 APPLICATION NUMBER: US/08/366,783
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: FABIAN, GARY
 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-POS/MS-DOS
SOTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
 109 aLysAla 111
 TELEPHONE: 415-324-0880
 TITILE OF INVENTION: Oil-Body Proteins As Carriers Of TITLE OF INVENTION: High-Value Peptides In Plants NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
 460 ATCCTCGTGCCGGCTCTCATCACCGTAGCACTTCTCATCACTGGCTTTCT 509
 93
 76 eLeuAlaPro.AsnArgTrpGlnGluIleLeuSerLeuIleIleSerPhe 92
23 lSerThrGlyAsnValAlaMet......
:|||:::|||::: |||
 ADDRESSEE: DEHLINGER & ASSOCIATES
STREET: 350 CAMBRIDGE AVENUE, SUITE 250
CITY: PALO ALTO
STATE: Callfornia
 COUNTRY: United States ZIP: 94025-1536
 REGISTRATION NUMBER:
 LeuThrIleSerAlaLeuLeuThr...AlaLeuLeuValThrGlyCysVa 23
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 SOFTWARE: PatentIn Ver. 2.1 SEQ ID NO 1
 GENERAL INFORMATION:
 Patent No.
 Sequence 1,
 TITLE OF INVENTION: GENE FOR ENZYME HAVING BOTH ALKALINE PULLULANASE AND TITLE OF INVENTION: ALKALINE ALPHA-AMYLASE ACTIVITIES FILE REFERENCE: 2173-105P
 EARLIER APPLICATION NUMBER: 08/952,084 EARLIER FILING DATE: 1997-11-10
 CURRENT APPLICATION NUMBER: US/09/514,302
CURRENT FILING DATE: 2000-02-28
 APPLICANT: KAWAI, Shuja APPLICANT: ITO, Susumu
 APPLICANT: OZAKI, Katsuya
APPLICANT: ARA, Katsutoshi
 APPLICANT:
 NUMBER OF SEQ ID NOS: 14
 5672 CACCACCAGGGGATGGGGATG...
 NAME/KEY:
LOCATION:
 ORGANISM:
 TYPE: DNA
5714CAGGCAACGGTAATGGCAATAATCCAGGAACACCACCAGGAAA 5756
 NAME/KEY: mat_peptide LOCATION: (241)..(595)
 NAME/KEY: sig_peptide
LOCATION: (145)..(240)
 FEATURE:
 FEATURE:
 FEATURE:
 LENGTH: 6142
 710
 610 GCAAGGATGAAGCTGGGAACCAAAGCTCAGGATATTAAAGACAGAGCTCA
 660 ATACTACGGACAGCAACATACAGGTGGTGAGCATGACCGTGACCGTACTC
 560 ATAAGTACGCAACGGGAGAGCACCCACAGGGGGTCAGATAAGTTGGACAGT 609
 510 CTCCTCTGGTGGGTTTGCCATTGCAGCTATAACCGTCTTCTCCTGGATCT
 57
 20 rGlyCysValSerThrGlyAsnValAlaMetLysGluGlnAsnGlnGlnT 37 ::: ::::::|||:::::|||:::
 70 LysPheGlyHisThrAlaIleLeuAlaProAsnArgTrpGln 83
 41 ThrIleIleLysGlyLysThrAsnLysGlnGluIleSerSerArg.PheG
 4 HisHisIleArgLeuThrIleSerAlaLeuLeuThrAlaLeuLeuValTh
 lySerAlaAspSer......IleSerPheMetIleValValIle 69
 GTGGTGGCCAGCACTACTATCGAAGGAAGAGCCATGGCGC 751
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 Quality:
Ratio:
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 Application US/09514302
 (145)..(5958)
 Bacillus sp
 KAWAI, Shuji
 IGARASHI,
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 21.239
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 40
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GENERAL INFORMATION:
APPLICANT: Selsted, Michael E.
APPLICANY: Tang, Yi-Quan
APPLICANY: Tang, Yi-Quan
APPLICANY: Tung, Jun
APPLICANY: Vuan, Jun
APPLICANY: Ouellette, Andre J.
TITLE OF INVENTION: Antimicrobial Theta Defensins and
FILE REFERENCE: P-UC 3095
CURRENT APPLICATION NUMBER: US/09/309,487
CURRENT FILING DATE: 1999-05-10
NUMBER OF SEQ ID NOS: 31
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 25
LENGTH: 2553
TYPE: DNA
ORGANISM: Macaca mulatta
US-09-309-487-25
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US-10-048-197-2 x US-09-309-487-25/rev
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 seq_documentation_block:
 seq_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-309-487-25
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 Percent Similarity:
 Patent No.
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 2362 ACTCCTCGTCTGCAAAGGCACCTCAAGCCTCTCGCTGACTCTGGGGACAC 2313
 2412 GTCAACCACGAAAAGCGCAGGACCCCAAACGCCTTTATAACAGTTGGCAA 2363
 5874
 5824
 5924 TCAGAAGAAAGCAGGATTGAAAGAAAAACCTTATAAA 5962
 55 gPheGlySerAlaAspSerIleSer.....PheMetIleV 67
 31 ysGluGlnAsnGlnGlnThrIleGluGlnThrIleIleLysGlyLysThr 47
 96
 87
 70 sPheGlyHisThrAlaIleLeuAlaProAsnArgTrpGlnGluIleLeuS 87
 54
 2 LeuAsnHisHisIleArgLeuThrIleSerAlaLeuLeuThrAlaLeuLe 18
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 AsnLysGlnGluIleSerSer..
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 5, Application US/09309487 6335318
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US-08-878-474-6
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 Ratio:
Percent Similarity:
 seq_documentation_block:
 Patent No.
 GENERAL INFORMATION:
APPLICANT: De Robertis, Edward M.
APPLICANT: BOUWMeester, Tewis
 INFORMATION FOR SEQ ID NO:
1367 AACTATCATGTAACTGTCCTCATAAGCTTGCTGTAGTTTAAAGTGCTCAT 1318
 APPLIANCE 18-JUN-13.
FILING DATE: 18-JUN-13.
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/020,150
APPLICATION NUMBER: US 60/020,150
APPLICATION NUMBER: US 60/020,150
 2093 CAAACACCTGAATGCACTCTTA 2072
 2143 GAGACTTATTCTCATTTGCTCTCATTTTTGTGCCTGTGCCCCATCAAACA 209.
 COUNTRY: U.S.A.
ZIP: 94111-4106
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
 2162
 FILING DATE: 20-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Siebert, J. Suzann
 SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
 SEQUENCE CHARACTERISTICS:
 TELECOMMUNICATION INFORMATION:
 TITLE OF INVENTION:
 CORRESPONDENCE ADDRESS:
 NUMBER OF SEQUENCES:
 100 oLysAsnLeuSerPheTyrLeu 107
 3 AsnHisHisIleArgLeuThrIleSerAlaLeuLeuThrAlaLeuLeuVa 19
 84 GluIleLeuSerLeuIleIleSerPheLeuTrpValLysProTyrArgPr 100
 67 alValIleLysPheGlyHisThrAlaIleLeuAlaProAsnArgTrpGln 83
 NAME: Siebert, J. Suzanne REGISTRATION NUMBER: 28,7! REFERENCE/DOCKET NUMBER:
 TELEPHONE:
 APPLICATION NUMBER:
 CITY: San Francisco
STATE: California
 LENGTH:
 STREET:
 ADDRESSEE:
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 /cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-878-474-6
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 415/362-5418
 Majestic,
 415/248-5500
 61.00
1.034
59.000
 double
 Factors
 Endoderm, Cardiac and Neural Inducing
 Parsons, Siebert & Hsue dero Center, Suite 1100
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 Version #1.25
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Ratio:
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SEQUENCE CHARACTERISTICS:
LENGTH: 507 base pairs
TYPE: nucleic acid
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ORIGINAL SOURCE:
STRAIN: dpd20
US-08-735-545-14
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 Percent Similarity:
 Sequence 14, Application US/08735545 Patent No. 6025131
 TITLE OF INVENTION: Iden
TITLE OF INVENTION: Pron
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: E. I. DU P
 GENERAL INFORMATION:
APPLICANT: Van Dy
 1120 GCAGTCAGTGGGTTGGGGCCCAAATCTTGGGCTTGTACCTCAAATTCGTA 1071
 1217 ATAGGCAACTCCTGCATTTACAGTAGTCAGAGGGGTAATAGTGATGGCTG 1168
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 REFERENCE/DOCKET NUMBER: CR-9989
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-892-8112
TELEFAX: 302-773-0164
 ATTORNEY/AGENT INFORMATION:
NAME: FLOYD, LINDA A.
REGISTRATION NUMBER: 33,
 SOFTWARE: MICROSOFT WORD 2.0C CURRENT APPLICATION DATA:
 COMPUTER READABLE FORM:
 APPLICANT:
 TITLE OF INVENTION:
 79 roAsnArgTrp......GlnGluIleLeuSerLeuIleIleSerPheLeu 93 ::::::|||| :::|||| ::::||||:::
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 46 LysThrAsnLysGlnGluIleSerSerArgPheGlySerAlaAspSerIl 62
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 MEDIUM TYPE: DISKETTE, 3.50 INCH
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MICROSOFT WINDOWS
 FILING DATE:
CLASSIFICATION:
 COUNTRY:
 APPLICATION NUMBER: US/08/735,545
 STREET:
 ADDRESSEE: AND COMPANY
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 WILMINGTON
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 UNITED STATES OF AMERICA
 Van Dyk, Tina K.
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 60.50
2.327
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 DU PONT DE NEMOURS
 Promoters
 Robert Alan
A Facile Method for
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 33,692
 Percent Identity:
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 3.1
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 TELEFAX: 302-773-0164
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 507 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
 Sequence 14, Application US/09449083 Patent No. 6194159
 GENERAL INFORMATION:
APPLICANT: Van Dy
APPLICANT: LaRoss
 TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
 ATTORNEY/AGENT INFORMATION:
NAME: FLOYD, LINDA A.
REGISTRATION NUMBER: 33,692
 COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.50 INCH
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MICROSOFT WINDOWS
SOFTWARE: MICROSOFT WORD 2.0C
CURRENT APPLICATION DATA:
 TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-892-8112
 CORRESPONDENCE ADDRESS:
ADDRESSEE: E. I. DU PONT DE NEMOURS
 142 CGCGACCGGCTCT...GCCTACGCGGAAAACAACGCGCAGACTACCAATG
 192 AGACTGAAGATTTCGAAAACTCTGCTGGCTGTAATGTTGACCTCTGCCGT 143
 40 lnThr 41
 23 lSerThrGlyAsnValAlaMetLysGluGlnAsnGlnGlnThrIleGluG 40
 95 AAAGC 91
 STREET: 1007 MAR CITY: WILMINGTON STATE: DELAWARE
 TOPOLOGY: lir
 REFERENCE/DOCKET NUMBER:
 APPLICATION NUMBER: FILING DATE:
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 ADDRESSEE:
 7 ArgLeuThrIleSerAlaLeuLeuThrAlaLeuLeuValThrGlyCysVa
 CLASSIFICATION:
 19898
 Quality:
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 dpd2090 lower
 1007 MARKET STREET
 UNITED STATES OF AMERICA
 LaRossa,
 Van Dyk,
 linear
 AND COMPANY
 DNA (genomic)
 60.50
2.327
74.286
 Robert Alan
A Facile Method for
Identifying Regulated
 Tina K.
 Promoters
 US/09/449,083
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; ORGANISM: Arabidopsis thaliana
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US-10-048-197-2 x US-08-868-373-3
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 seq_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-08-868-373-3
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 Percent Similarity:
 Align seg 1/1 to reverse of: US-09-449-083-14 from: 1
 GENERAL INFORMATION:
APPLICANT: Jaworski, Jan G.
 Sequence 3, Application US/08868373 Patent No. 6307128
 CURRENT APPLICATION NUMBER: US/08/868,373
CURRENT FILING DATE: 1997-06-03
NUMBER OF SEQ ID NOS: 22
 APPLICANT: Post-Beittenmiller, Martha A. APPLICANT: Todd, James
TITLE OF INVENTION: FATTY ACID ELONGASES
FILE REFERENCE: 07148/064001
 SOFTWARE: FastSEQ for Windows Version 3.0
 1349
 1303
 1156 TGTATCCATGCGGGTGGTAGAGCGCTAATTGATGAGAATGGAGAAGAATCT 1205
 1206 TCATCTAACTCCACTAGACGTTGAGGCTTCAAGAATGACATTA...CACA 1252
 93
 65
 55
 22 CysValSerThrGlyAsnValAlaMetLysGluGlnAsnGlnGlnThrIl 38
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 alignment_scores:
 5225348-2
 CONTAINING THE DNA FRAGMENT
NUMBER OF SEQUENCES: 9
CURRENT APPLICATION DATA:
 ;Patent No. 5225348
;Patent No. 5225348
; APPLICANT: HAGATA, SHIGEKAZU;SUGANO,
;UETSUKI, TAICHI;KAZIRO, YOSHITO
; TITLE OF INVENTION: DNA FRAGMENT AND
 Sequence 49, Application US/08484101B
Sequence 49, Application US/08484101B
Patent No. 5824868
GENERAL INFORMATION:
GENERAL INFORMATION: Institute of Technology
APPLICANT: California Institute of Technology
TITLE OF INVENTION: PLANTS HAVING MODIFIED RESPONSE TO
TITLE OF INVENTION: ETHYLENE
 Align seg 1/1 to: 5225348-2
 Percent Similarity:
 SEQ ID NO:2:
 NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: Richard F. Trecartin
STREET: 3400 Embarcadero Center, Suite 3400
 TITLE OF INVENTION:
 556
 456
 406
 606 GGCTACAACCCCGACACAGTAGCATTT 632
 506 AATTGTCGGTGTTAACAAATGGATTCCACTGAGCCACCCTACAGCCAGA
 306 ACCAGGAAGTACTATGTGACTATCATTGATGCCCCAGGACACAGAGACTT
 356 TATCAAAAACATGATTACAGGGACATCTCAGGCTGACTGTGCTGTCCTGA 405
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 97
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 38 leGluGlnThrIleIleLysGlyLys.....
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 APPLICATION NUMBER: US/07/447,823 FILING DATE: 08-DEC-1989
 STATE:
 CITY:
 COUNTRY:
 LENGTH: 1753
 snArgTrpGlnGluIleLeuSerLeuIleIleSerPheLeuTrpValLys 96
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 CAGACCCGAGAGCATGCCCTTCTGGCTTACACACTGGGTGTGAAACAACT 505
 TIGTIGCTGCTGGTGTTGGTGAATTTGAAGCTGGTATCTCCAAGAATGGG 455
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COMPUTER READABLE FORM:

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US-08-484-1018-49
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seq_documentation_block:
 Ratio:
Percent Similarity:
 Align seg 1/1 to: US-08-484-1018-49
 TELEFAX: (415) 398-3249 INFORMATION FOR SEQ ID NO:
 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,101B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
 395
 345
 APPLICATION NUMBER: PCT/US94/
FILING DATE: 01-UUL-1994
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
 445 GG 446
 245 AAAGTTACTAAAAATTTTTGATTCTTTGGGACGAAACGAGATAATGGAAT 294
 FEATURE:
 SEQUENCE CHARACTERISTICS:
 ATTORNEY/AGENT INFORMATION:
NAME: Trecartin, Richard F.
 REGISTRATION NUMBER: 31,801
REFERENCE/DOCKET NUMBER: A-57515-2/RET
FELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
 49
 82
 22 CysValSerThrGlyAsnValAlaMetLysGluGlnAsnGlnGlnThr..
 APPLICATION NUMBER: US 08/086,555 FILING DATE: 01-JUL-1993 CLASSIFICATION: 800
 MEDIUM TYPE: Floppy disk
COMPUTER: IRM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0
 LENGTH: 2405 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
 TELEPHONE:
 TOPOLOGY:
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288..2196
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 Release #1.0, Version
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 Percent
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 from: 1
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 2405
 37
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seq_documentation_block:
 Sequence 19, Application US/09058489
 Patent no. 6103886
 GENERAL INFORMATION:
 APPLICANT: Whitehead Institute for Biomedical Research
 APPLICANT: Laho, Bruce
 APPLICANT: Page, David
 alignment_block:
US-10-048-197-2 x US-08-714-524D-49
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; LOCATION: (288)..(2195)
US-08-714-524D-49
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 Align seg 1/1 to: US-08-714-524D-49
 Percent Similarity:
 SOFTWARE: PatentIn Ver. 2.1 SEQ ID NO 49
 GENERAL INFORMATION:
 Sequence 49, Application US/08714524D Patent No. 6294716
 TITLE OF INVENTION: Genes in the No. 6103886-Recombining Region of TITLE OF INVENTION: the Y Chromosome FILE REFERENCE: WHI97-08pA CURRENT APPLICATION UNMBER: US/09/058,489 CURRENT FILING DATE: 1998-04-10 EARLIER APPLICATION NUMBER: 60/041,877 EARLIER FILING DATE: 1997-04-11
 CURRENT APPLICATION NUMBER: US/08/714,524D CURRENT FILING DATE: 1996-09-16 NUMBER OF SEQ ID NOS: 56
 TITLE OF INVENTION: PLANTS HAVING MODIFIED RESPONSE TO ETHYLENE FILE REFERENCE: a-57515-4
 APPLICANT:
 APPLICANT: Meyerowitz, Elliott M
NUMBER OF SEQ ID NOS: 91
 ORGANISM: Lycopersicon esculentum FEATURE:
 LENGTH: 2405
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 395 GTTGGAGCTTATTTATTTTGTCCACAAATCTGCATGCTTCCCATACAGAT 444
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 82 rp
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 Chang, Caren
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; Patent No. 6103886
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 Percent Similarity:
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 EARLIER APPLICATION NUMBER: 60/041,877
EARLIER FILING DATE: 1997-04-11
NUMBER OF SEQ ID NOS: 91
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 20
 SEQ ID NO 19
 GENERAL INFORMATION:
 APPLICANT: Whitehead Institute for Biomedical Research APPLICANT: Lahn, Bruce APPLICANT: Lahn, Bruce APPLICANT: David TITLE OF INVENTION: Genes in the No. 6103886-Recombining Region TITLE OF INVENTION: the Y Chromosome FILE REFERENCE: WHI97-08pA CURRENT APPLICATION NUMBER: US/09/058,489 CURRENT FILING DATE: 1998-04-10
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EARLIER FILING DATE: 1997-04-11
NUMBER OF SEQ ID NOS: 91
SOFTWARE: FastSEQ for Windows Version 3.0
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LENGTH: 6476
TYPE: DNA
ORGANISM: Human
US-09-058-489-21
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Percent Similarity:
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 GENERAL INFORMATION:
 Patent No.
 APPLICANT: Whitehead Institute for Biomedical Research APPLICANT: Lahn, Bruce APPLICANT: Lahn, Bruce APPLICANT: Page, David TITLE OF INVENTION: Genes in the No. 6103886-Recombining TITLE OF INVENTION: the Y Chromosome FILE REFERENCE: WHI97-08pA CURRENT APPLICATION NUMBER: US/09/058,489 CURRENT FILING DATE: 1998-04-10
 Sequence 21, Application US/09058489
Patent No. 6103886
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 57 GlySerAlaAspSerIleSerPheMetIleValValIleLysPheGlyHi
 25 rGlyAsnValAlaMetLysGluGlnAsnGlnGlnThrIle.....GluG
 9 ThrIleSerAlaLeuLeuThrAlaLeuLeuValThrGlyCysValSerTh
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Percent Identity: 26.000
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 6476
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 of.
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Quality:
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Percent Similarity:
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US-07-961-522-3
Align seg 1/1 to: US-07-961-522-3
 Sequence
 GENERAL INFORMATION:
 TELEPHONE: (415) 617-89
TELEFAX: (415) 327-3231
INFORMATION FOR SEQ ID NO:
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 APPLICANT:
APPLICANT:
APPLICANT:
 tent No.
 2764 AACTCCGCTCAGGGGCTTCAT.
 2714 ATACAGACCTGAACAGCAGCACAGAAGAGCCATGGAGAAAACAGCTATCT 2763
 COMPUTER READABLE FORM:
MEDIJUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
 NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESSE: ROBERTA L. ROBINS
STREET: 635 BRYANT STREET
 SEQUENCE CHARACTERISTICS:
 TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 617-8999
 ATTORNEY/AGENT INFORMATION:
 APPLICANT: ROSSI-CAMPOS, AMALIA
TITLE OF INVENTION: VACCINES FOR ACTINOBACILLUS
TITLE OF INVENTION: PLEUROPNEUMONIAE
 FEATURE:
 MOLECULE TYPE: DNA (genomic)
 90
 73
 57
 NAME: ROBINS, ROBERTA L. REGISTRATION NUMBER: 33, REFERENCE/DOCKET NUMBER:
 STRANDEDNESS:
 CLASSIFICATION:
 APPLICATION NUMBER: US
FILING DATE: 19921015
 COUNTRY:
 CITY: PALO ALTO
 NAME/KEY:
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 leSerPheLeuTrpValLysProTyrArgProLysAsnLeuSerPheTyr 106
 3, Application US/07961522
3, 5417971
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 CALIFORNIA
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 WILLSON, PHILIP J.
 POTTER, ANDREW A.
 UNITED STATES OF AMERICA
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 59.00
 US/07/961,522
 33,208
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 Gaps:
Percent Identity:
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from: 1
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: 27.632
 1903
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 Patent No.
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SEQUENCE CHARACTERISTICS:
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 CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Robins, Roberta L.
 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: 22-MAR-199
 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
 APPLICANT: ROSSI-Campos, Amalia
TITLE OF INVENTION: ACTINOBACILLUS PLEUROPNEIMONIAE
TITLE OF INVENTION: TRANSFERRIN BINDING PROTEINS AND
NUMBER OF SEQUENCES: 11
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 TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-617-8999
TELEFAX: 415-327-3231
 CORRESPONDENCE ADDRESS:
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 APPLICANT:
 APPLICANT:
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 52 eSerSerArgPheGlySerAlaAspSerIleSerPheMetIleValValI 69
 38 IleGluGlnThrIleIle.....LysGlyLysThrAsnLysGlnGluIl 52
 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
 NAME/KEY:
 TOPOLOGY:
 STRANDEDNESS:
 TYPE:
 REFERENCE/DOCKET NUMBER:
 NAME: Robins, Roberta
REGISTRATION NUMBER: :
 COUNTRY:
 CITY: Palo Alto
 ADDRESSEE:
 ENGTH:
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DEDNESS: single
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 California
 1903 base pairs
 635 Bryant
 USA
 Potter, Andrew A. Gerlach, Gerald F. Willson, Philp J.
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 CDS
 linear
 Reed & Robins
 22-MAR-1994
 TRANSFERRIN BINDING PROTEINS AND USES THEREOF
 US/08/217,438
 33,208
 <u>ω</u>
 9001-0015.01
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alignment\_scores:

Quality: Ratio: Percent Similarity:

59.00 1.439 53.947

Percent Identity:

76 4 27.632

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 TELEFAX: (415) 327-32
INFORMATION FOR SEQ ID NO:
 1051
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 MEDIUM TYPE: floppy disk
COMPOTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
 APPLICANT:
 928
 REGISTRATION NUMBER: 33,208
REFERENCE/FOCKET NUMBER: 90
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 327-3400
 CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
 SEQUENCE CHARACTERISTICS:
 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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 APPLICANT:
 97
 52
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 ITLE OF INVENTION: VACCINES FOR ACTINOBACILLUS ITLE OF INVENTION: PLEUROPNEUMONIAE
 TOPOLOGY:
 APPLICATION NUMBER: FILING DATE: 12-007
 NAME/KEY:
 COUNTRY:
 CITY: PALO ALTO
 STREET:
 STRANDEDNESS:
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 INFORMATION:
 3, Application US/08321978
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 nucleic acid
DEDNESS: double
 ROBINS, ROBERTA
 CALIFORNIA
 285 HAMILTON AVE, SUITE 200
 GERLACH, GERALD F. WILLSON, PHILIP J.
 ROSSI-CAMPOS, AMALIA
 POTTER, ANDREW A.
 CDS
 UNITED STATES OF AMERICA
 12-OCT-1994
 DNA (genomic)
 327-3231
NO: 3:
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 APPLICANT: APPLICANT:
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APPLICATION NUMBER: US 08/321,978
FILING DATE: 12-OCT-1994
ATTORNEY/AGENT INFORMATION:
 SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/710,584
 COMPUTER READABLE FORM:
 CORRESPONDENCE ADDRESS:
ADDRESSEE: ROBERTA L
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 REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 90
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 327-3400
 TITLE OF INVENTION:
 878 TTGCAGGCAACCGTTTTAGGGGAAAAGCCAAAGCAGAAAAAGCAGGTGAT
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 52 eSerSerArgPheGlySerAlaAspSerIleSerPheMetIleValValI 69
 38 IleGluGlnThrIleIle.....LysGlyLysThrAsnLysGlnGluIl
 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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 FILING DATE:
 MEDIUM TYPE:
 COUNTRY:
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 Application US/08710584
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 UNITED STATES OF AMERICA
 GERLACH, GERALD F.
WILLSON, PHILIP J.
ROSSI-CAMPOS, AMALIA
VENTION: VACCINES FOR ACTINOBACILLUS
 POTTER, ANDREW A.
 ROBERTA L.
 Floppy disk
 59.00
1.439
53.947
 327-3231
 PLEUROPNEUMONIAE
 ROBINS
 Length: 76
Gaps: 4
Percent Identity: 27.632
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 9001-0015.02
 from:
 104
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to
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 950
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STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)

LENGTH: 1903 base pairs

nucleic acid

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US-08-710-584-3
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US-10-048-197-2 x US-08-710-584-3
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 Align seg 1/1 to: US-08-710-584-3 from: 1 to:
 Ratio:
Percent Similarity:
 SOFTWARE: PatentIn Ver. 2
SEQ ID NO 223
LENGTH: 2908
TYPE: DNA
ORGANISM: Pan troglodytes
 Sequence 223, Application US/09564805 Patent No. 6333403
 APPLICANT: Tavtigia
 APPLICANT: Tavtigian, Sean V.
APPLICANT: Teng, David H.F.
APPLICANT: Simard, Jacques
APPLICANT: Rommens, Johanna M.
APPLICANT: Myriad Genetics, Inc.
TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
FILE REFERENCE: 2318-258
 CURRENT APPLICATION NUMBER: US/09/564,805
CURRENT FILING DATE: 2000-05-05
PRIOR APPLICATION NUMBER: US 60/107,468
PRIOR FILING DATE: 1998-11-06
PRIOR APPLICATION NUMBER: 09/434,382
PRIOR FILING DATE: 1999-11-05
NUMBER OF SEQ ID NOS: 240
FEATURE:
NAME/KEY: CDS
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Percent Identity: 27.632
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 GENERAL INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
 1429 AGAAGTCAGTACCCAGAAATCATCTTCCTTGGAACAGGGTCTGCCATCCC 1478
 REFERENCE/DOCKET NUMBER: B9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)343-4341
 ATTORNEY/AGENT INFORMATION:
 CORRESPONDENCE ADDRESS
 NUMBER OF SEQUENCES:
 TITLE OF INVENTION:
 APPLICANT:
 APPLICANT:
 APPLICANT:
 66
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 38 eGluGlnThrIleIleLysGlyLysThrAsnLysGlnGluIleSerSerA 55
 22 CysValSerThrGlyAsnValAlaMetLysGluGlnAsnGlnGlnThrI1
 TYPE: nucleic acid
 NAME: Osman, Richard A. REGISTRATION NUMBER: 36
 APPLICATION NUMBER: US/08/121,713D FILING DATE: 13-SEP-1993 CLASSIFICATION: 514
 STREET: 268 Busn our CITY: San Francisco
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 STRANDEDNESS:
 COUNTRY:
 ADDRESSEE:
 ENGTH:
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 94104
 Quality:
 Ratio:
 CA
 E: SCIENCE & TECHNOLOGY LAW GROUP 268 Bush Street, Suite 3200
 3560 base pairs
 Matthes, David
Bentley, David R.
O'Connor, Timothy
OVENTION: The Semaphorin Gene Family
 Goodman, Corey S. Kolodkin, Alex L.
 (415) 343-4342
 USA
linear
 59.00
1.686
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 36,627
 Percent Identity: 26.027
 B94-002-1
 from: 1
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 38
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CDNA

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GENERAL INFORMATION:
APPLICANT: Goodman, Corey S.
APPLICANT: Kolodkin, Alex L.
APPLICANT: Matthes, David R.
APPLICANT: Bentley, David R.
APPLICANT: O'Connor, Timothy
TITLE OF INVENTION: The Semaphorin Gene Family
NUMBER OF SEQUENCES: 100
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 768 Bush Street Gitt 2700
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 ZIP: 94104
 STATE:
 ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP STREET: 268 Bush Street, Suite 3200
 COUNTRY:
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 Quality:
 San Francisco
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 USA
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 Version
 from: 1
 to: 3560
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 104 rPheTyrLeu 107
 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/0
FILING DATE: 13-SEP-1993
ATTORNEY/AGENT INFORMATION:
 FEATURE:
 TOPOLOGY: li
 TELEPHONE: (415)343-4341
 89
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 39 luGlnThrIleIleLysGlyLysThrAsnLysGlnGlu.IleSerSerAr 55
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 TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear .
 NAME: Osman, Richard A. REGISTRATION NUMBER: 36, REFERENCE/DOCKET NUMBER:
 TELEX:
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 CLASSIFICATION:
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Kolodkin, Alex
Bentley,
 Matthes,
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ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A.
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: B94
TELECOMMUNICATION INFORMATION:
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TELEPHONE: (415)343-4342
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
 NUMBER OF SEQUENCES: 100
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 Bush Street, Suite 3200
 FEATURE:
 TOPOLOGY: linear MOLECULE TYPE: cDNA
 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/121,713
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 CITY: San Francisco
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 Quality:
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 O'Connor, Timothy
WENTION: The Semaphorin Gene Family
 USA
 CDS
 Floppy disk
 59.00
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 NAME: Osman, Richard A.
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: B9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)343-4341
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
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ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 Bush Street, Suite 3200
 APPLICATION NUMBER: US 08/121,713
FILING DATE: 13-SEP-1993
ATTORNEY/AGENT INFORMATION:
 104 rPheTyrLeu 107
 APPLICANT: Bentley APPLICANT: O'Conno TiTLE OF INVENTION:
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 FILING DATE: CLASSIFICATION:
 CITY: San Francisco
 STRANDEDNESS:
 TELEFAX: (415) 343-4342
 APPLICATION NUMBER:
 Quality:
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 Ratio:
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 3560 base pairs
 O'Connor, Timothy
WENTION: The Semaphorin Gene Family
 USA
 Kolodkin, Alex
Matthes, David
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 CDS
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 Bentley, David R.
 linear
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 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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CURRENT APPLICATION DATA:
 APPLICANT: Goodman, Corey S. APPLICANT: Kolodkin, Alex L. APPLICANT: Matthes, David
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CORRESPONDENCE ADDRESS:
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 PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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 NAME: Osman, Richard REGISTRATION NUMBER:
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 San Francisco
 94104
 CA
 268 Bush Street, Suite 3200
 Matthes, David
Bentley, David R.
 USA
 O'Connor, Timorny
VENTION: The Semaphorin Gene Family
 (415) 343-4342
 SCIENCE & TECHNOLOGY LAW GROUP
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, Richard A.
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 08/835,268
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 Align seg 1/1 to reverse of: US-09-060-610-59
 Percent Similarity:
 APPLICATION NUMBER: PCT/US94/
FILING DATE: 13-SEP-1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Osman, Richard A.
REGISTRATION NUMBER: 36,627
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CITY: San
STATE: CA
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REFERENCE/DOCKET NUMBER: FP
 ADDRESSEE: FLEHR HOHBACH TEST ALBRITTON & HERBERT STREET: 4 Embarcadero Center, Suite 3400 CITY: San Francisco
 CA
 Ratio:
 The Regents of the University of California VENTION: The Semaphorin Gene Family
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 PCT/US94/10151A
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 from: 1
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TELEPHONE:

(415)

(415) 781-1989 15) 398-3249

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Sequence 1, Application US/09007999

Patent No. 6087559

GENERAL INFORMATION:
APPLICANT: NICHOLS, Scott E.
TITLE OF INVENTION: Substitutes for Modified Starch and TITLE OF INVENTION: Latexes in Paper Manufacture FILE REFERENCE: 0356D

CURRENT APPLICATION NUMBER: US/09/007,999

CURRENT FILING DATE: 1998-01-16

EARLIER APPLICATION NUMBER: 08478,704

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EARLIER FILING DATE: 1995-06-07

INUMBER OF SEQ ID NOS: 2

SOFTWARE: FastSEQ for Windows Version 3.0

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 FEATURE:
 TOPOLOGY: linear
MOLECULE TYPE: cDNA
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 39 luGlnThrIleIleLysGlyLysThrAsnLysGlnGlu.IleSerSerAr 55
 72 lyHisThrAlaIleLeuAlaProAsnArgTrpGlnGluIleLeuSerLeu 88
 55 gPheGlySerAlaAspSerIleSerPheMetIleValValIleLysPheG 72
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EARLIER FILING DATE: 1995-06-07
EARLIER APPLICATION NUMBER: 09/009,620
EARLIER FILING DATE: 1998-01-20
EARLIER APPLICATION NUMBER: 08/485,243
EARLIER FILING DATE: 1995-06-07
 TITLE OF INVENTION: Substitutes for Modified Starches TITLE OF INVENTION: Latexes in Paper Manufacture FILE REFERENCE: 0357CR CURRENT APPLICATION NUMBER: US/09/210,361 CURRENT FILING DATE: 1998-12-11
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CC and to DNA encoding them (AAF59778 and AAF59779, respectively). The
CC invention also relates to immunogenic fragments of the BASB122 and
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CC BASB124 nucleic acids, the recombinant production of BASB122 or
CC COMPASB124, vaccine compositions comprising the BASB122 or BASB122 or
CC compositions comprising an antibody against BASB122 or BASB124 proteins
CC compositions comprising a Moraxella Catarrhalis infection via the
CC detection of BASB122 or BASB124 proteins or antibodies. The vaccine
CC compositions of the invention are useful as prophylactic or therapeutic
CC agents against Moraxella catarrhalis infections in mammals, particularly
CC humans. Moraxella catarrhalis is a Gram negative bacterium frequently
CC isolated from the human upper respiratory tract, which is responsible for
CC several pathological conditions. It is responsible for about 15% of
CC onsocomial infections and, less frequently, invasive diseases. BASB122 or
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 Claim 13; Page 66; 75pp; English.
 against bacterial infections, e.g. otitis media
 New BASB122 and BASB124 polypeptides and polynucleotides from Moraxella catarrhalis strain ATCC 43617, useful as therapeutic agents or vaccines
 WPI; 2001-159874/16.
P-PSDB; AAB60640.
 Thonnard
 30-JUL-1999;
30-JUL-1999;
 08-FEB-2001.
 Moraxella catarrhalis
 Moraxella catarrhalis strain ATCC43617 BASB122 DNA.
 02-MAY-2001 (first entry)
 31-JUL-2000; 2000WO-EP07365
 (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
 4
 The present sequence represents strain ATCC43617 BASB122 protein
 99GB-0018034.
99GB-0018036.
 DNA
 or
 encoding
 pneumonia
 67.50
67.00
67.00
67.00
67:00
 108.34
134.79
129.96
129.53
128.84
 36.85
68.41
72.35
79.06
```

Sequence 336

BP; 106

A; 65 C;

61 G; 104 T; 0 other;

```
seq_documentation_block:
ID AAF28551 standard;
 seq_name:
 alignment_scores
 Align seg 1/1 to: AAF59778
 US-10-048-197-2 x AAF59778
 Percent Similarity: 100.000
 Genomic library for identifying diagnostic and therapeutic compositions, and for identifying virulence factors, regulatory elements and drug targets, comprises Moraxella catarrhalis nucleacids -
 Genomic library; bacteria; human upper airway; otitis media; sinusitis; bronchopulmonary; endocarditis; meningitis; ss.
 101
 Moraxella catarrhalis.
 Genomic fragment #38
 04-APR-2001
 301
 151
 Lagace RE,
 18-JUN-1999;
 28-DEC-2000
 WO200078968-A2
 101
 251
 201
 (INCY-) INCYTE GENOMICS INC
 16-JUN-2000;
 84
 67
 51
 34
 51
 17
 snGlnGlnThrIleGluGlnThrIleIleLysGlyLysThrAsnLysGln 50
 uLeuValThrGlyCysValSerThrGlyAsnValAlaMetLysGluGlnA 34
 TTTGGTAACAGGTTGTGTTTCTACTGGTAATGTTGCAATGAAAGAGCAAA 100
 ACCAACAAACCATTGAGCAGACCATCATTAAGGGCAAGACCAATAAGCAA 150
 2001-041427/05
 /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:AAF28551
 Quality:
Ratio:
 Patterson
 2000WO-US16649
 (first entry)
 9908-0140121
 558.00
5.027
 DNA;
 Ç
 94750
 from:
 Berg
 Percent Identity:
 č
 ۳
 .
6
 Length:
Gaps:
 100.000
 250
 84
 200
 67
```

÷

Neisseria meningitidis

```
seq_documentation_block:
ID AAV03597 standard; DN
XX
AC AAV03597;
XX
DT 22-OCT-1998 (first e
XX
Neisseria meningitidi
XX
N. gonorrheae; N. lac
KW region 3; pathogenici
XW meningitis; ss.
XX
OS Neisseria meningitidi
XX
NS Wo9802547-A2.
 alignment_block:
US-10-048-197-2 x AAF28551
 alignment_scores:
 seq_name: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:AAV03597
 Quality: 558.00
Ratio: 5.027
Percent Similarity: 100.000
 Align seg 1/1
 75467
 75517
 75417
 75367
 75317
 75267 ATGTTAAATCATCATATTCGCCTGACTATTTCCGCTTTACTGACGGCACT 75316
 75567
 The present invention relates to a Moraxella catarrhalis genomic library comprising of a combination of 41 nucleic acid molecules (see AAF28514-AAF2854). The library has a number of uses described in the specification e.g. is useful for aidentifying diagnostic and therapeutic compositions. M. catarrhalis (Branhamella catarrhalis) is a large
 101
 N. gonorrheae; N. lactami
region 3; pathogenicity;
 AAV03597 standard; DNA;
 Sequence 94750 BP; 27128 A; 18811 C; 21444 G; 27367 T; 0 other
 aerobic, gram-negative diplococcus, normally found among the bacterial flora of human upper airways. M. catarrhalls is known to cause acute, localised infections such as otitis media, sinusitis and bronchopulmonary infection and life-threatening, systemic diseases including endocarditis
 Claim 1; Page 415-436; 545pp; English
 Neisseria meningitidis DNA sequence
 84
 67
 51
 34
 17
 uLeuValThrGlyCysValSerThrGlyAsnValAlaMetLysGluGlnA 34
 GluIleSerSerArgPheGlySerAlaAspSerIleSerPheMetIleVa
 meningitis.
 AAGAACTTGTCATTTTATTTGACAGCAAAGGCA
 LysAsnLeuSerPheTyrLeuThrAlaLysAla 111
 AAATTTTATCCCTTATAATTTCTTTTCTTTTGGGTGAAACCATACAGACCA 75566
 GAGATTTCTAGTAGATTTGGTTCTGCTGATAGCATCTCTTTTATGATAGT
 ACCAACAAACCATTGAGCAGACCATCATTAAGGGCAAGACCAATAAGCAA
 snGlnGlnThrIleGluGlnThrIleIleLysGlyLysThrAsnLysGln
 TTTGGTAACAGGTTGTGTTTCTACTGGTAATGTTGCAATGAAAGAGCAAA
 luIleLeuSerLeuIleIleSerPheLeuTrpValLysProTyrArgPro 100
 lValIleLysPheGlyHisThrAlaIleLeuAlaProAsnArgTrpGlnG
 to:
 (first entry)
 lactamica;
 267
 ica; chromosome Z2491; region 1;
blood-brain barrier; diagnosis;
 from:
 Length: 111
Gaps: 0
Percent Identity: 100.000
 ВP
 .
6
 E29
 75599
 94750
 75366
 50
 67
 84
 region 2; infection;
```

```
alignment_scores:
Quality:
Ratio:
Percent Similarity:
 alignment_block:
US-10-048-197-2 x AAV03597
 Align seg 1/1 to: AAV03597
 AAV03575-606 represent sequences that are present in Neisseria meningitidis and N. gonorrheae but not in N. lactamica, except for the genes involved in biosynthesis of the capsule polysaccharide, frpA or C, opc, porA, rotamase, sequence IC1106, IgA protease, pillin, pilC, proteins which bind transferrin and opacity proteins. The DNA sequences are responsible for the differences in pathogenicity between N. meningitidis and N. gonorrheae, specifically they include the genes that allow N. meningitidis to cross the blood-brain barrier. DNA sequences common to N. meningitidis and N. gonorrheae, but absent from N. lactamica, are responsible for colonisation and penetration of the mucosa. The DNA sequences can be used to produce probes and primers, and antibodies produced against the encoded proteins are used in standard hybridisation/immunoassay processes for diagnosis of N. meningitidis
 Genes present in Neisseria meningitidis but not other Neisseria species - and related host cells, RNA, anti-sense sequences, polypeptide(s) and antibodies, useful for diagnosing Neisseria meningitidis infection and in protective vaccines
 WPI; 1998-110594/10
 (INRM) INSERM INST NAT SANTE & RECH MEDICALE. (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN. (SMIK) SMITHKLINE BEECHAM.
211
 161
 111
 Sequence 267 BP;
 Example 4; Page 125; 150pp; French.
 22-JAN-1998
 11-JUL-1997;
 40
 infection, particularly meningitis.
 73
 57
 64
 23
 14
 lnThrIleIleLysGlyLysThrAsnLysGlnGluIleSerSerArgPhe 56
 CGCATCATCGTTTCGGCTGCGTTCGTTGGCATTAGCAGGTTGCGG
CAATGCTATGTTA 223
 AATGAAGGCATACGCATCAACTTTACCGCAACTGTGGGTAAGCGCGTGAC
 CCGCGTTTGCCTTGGGCGTCACCAATGCCGTAAAAATCAGCAACCGCAGC
 CTCAATCAATAATGTAACCGTTTCCGACCAGAAACTTCAGGAA...CGTG
 ArgLeuThrIleSerAlaLeuLeuThrAlaLeuLeuValThrGlyCysVa
 sThrAlaIleLeu
 GlySerAlaAspSerIleSerPheMetIleValValIleLysPheGlyH1 73
 ű×
 Tinsley C,
 97WO-FR01295
 80.50
1.677
67.606
 71 A; 70
 77
 Achtman M,
 from: 1
 C; 61 G;
 Percent
 .
6
 Identity:
 65
 Merker P,
 Length:
 267
 T;
0
 other;
 33
 Ruelle
 21
 160
 40
 63
 23
```

seq\_documentation\_block:

seq\_name:

/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:AAA15394

```
alignment_scores:
Quality:
Ratio:
 $\times \times \
 alignment_block:
US-10-048-197-2 x AAA15394
 Align seg 1/1
 Percent Similarity:
 Aujame L, r
 The present sequence represents a genomic fragment of Neisseria meningitidis. The specificatino describes proteins that are specific for pathogenic strains of Neisseria. The polynucleotides, polypeptides, or their antigenic fragments, are used in vaccines to treat or protect against Neisseria infections, particularly by N. meningitidis. The polynucleotide sequences are also used for recombinant production of the polypeptide and to produce attenuated Neisseria strains that overexpress it, or express it in a non-toxic mutant form.

note: the present sequence is included in Claim 1, but it is those sequences that do not include the present sequence that are actually
 111
 Sequence 267
 Claim 1; Page 43; 187pp; French.
 New polypeptide specific or preventative vaccines
 WPI;
161
 (INMR) PASTEUR MERIEUX SERUMS & VACCINS SA.
 30-OCT-1998;
 28-OCT-1999;
 11-MAY-2000.
 WO200026375-A2
 Neisseria meningitidis.
 Pathogenic strain; Neisseria; vaccine; Neisseria infection;
 Genomic
 04-SEP-2000
 AAA15394 standard; DNA; 267 BP.
 57
 40
 64
 14
 23 lSerThrGlyAsnValAlaMetLysGluGlnAsnGlnGlnThrIleGluG
 7 ArgLeuThrIleSerAlaLeuLeuThrAlaLeuLeuValThrGlyCysVa
 CCGCGTTTGCCTTGGGCGTCACCAATGCCGTAAAAATCAGCAACCGCAGC
 CGCATCATCGTTTCGGCTGCGTTGCGTTGCGTTAGCAGGTTGCGG
AATGAAGGCATACGCATCAACTTTACCGCAACTGTGGGTAAGCGCGTGAC
 CTCAATCAATAATGTAACCGTTTCCGACCAGAAACTTCAGGAA...CGTG
 GlySerAlaAspSerIleSerPheMetIleValValIleLysPheGlyHi
 fragment of Neisseria
 to: AAA15394
 Bouchardon
 Perrin
 BP;
 (first
 98FR-0013693
 99WO-FR02643
 80.50
1.677
67.606
 71
 Ą;
 entry)
 70
 for pathogenic Neisseria useful in therapeutic and for diagnosis -
 from:
 Ç
 Percent Identity:
 Renauld-Mongenie
 61
 meningitidis 22491
 G;
 diagnosis
 .
6
 65
 T; 0 other;
 ō
 33.803
 Rokbi
 ₿,
 160
 40
 56
 63
210
 Nassif
 ×
```

73

sThrAlaIleLeu

77

```
seq_documentation_block:
ID AAA76029 standard; DN
XX
AC AAA76029;
XX 19-JAN-2001 (first e
DE Neisseria meningitidi
XX BASB059; respiratory
KW BASB059; respiratory
KW bacteraemia; meningitidi
XX Neisseria meningitidi
XX New Dacteraemia; meningitidi
XX New Dacteraemia; meningitidi
XX New Dacterian and treatme
XX (SMIK) SMITHKLINE BE
XX SMIK) SMITHKLINE BE
XX New Isolated polypept
PT detection and treatme
XX Claim 7; Page 61; 77p
XX New Isolated polypept
PT detection and treatme
XX Claim 7; Page 61; 77p
XX New Isolated polypept
PT detection and treatme
XX Claim 7; Page 61; 77p
XX The present sequence
CC gene, its protein, ag
CC assays for the bacter
CC The present for bacter
CC Invasive bacterial di
XX Sequence 339 BP; 93 A
 alignment_scores:
Quality:
 alignment_block:
 seq_name: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:AAA76029
 Align seg 1/1 to:
 US-10-048-197-2 x AAA76029
 Ratio:
Percent Similarity:
 The present sequence is the Neisseria meningitidis BASB059 gene. Th gene, its protein, agonists and antagonists can be used in diagnost assays for the bacterium, as vaccines to prevent infection and as treatments for bacterial infection, particularly those caused by Neisseria meningitidis, such as upper respiratory tract infections, invasive bacterial diseases, bacteraemia and meningitis.
 Claim 7; Page 61; 77pp; English.
 New isolated polypeptide from Neisseria meningitidis detection and treatment of N. meningitidis infection {\bf r}
 25-JAN-2000; 2000WO-EP00561
 AAA76029 standard; DNA;
 (SMIK) SMITHKLINE BEECHAM BIOLOGICALS
 Neisseria meningitidis.
 Neisseria meningitidis BASB059 gene.
 211
60 CTCAATCAATAATGTAACCGTTTCCGACCAGAAACTTCAGGAACGTGCCG
 10
 23 ISerThrGlyAsnValAlaMetLysGluGlnAsnGlnGlnThrIleGluG
 CGCATCATCGTTTCGGCTGCGTTCGTTGGCGTTGGCATTAGCAGGTTGCGG
 CAATGCTATGTTA 223
 ArgLeuThrIleSerAlaLeuLeuThrAlaLeuLeuValThrGlyCysVa
 respiratory tract infection;
 meningitis; ds.
 (first entry)
 AAA76029
 99GB-0002070
 80.00
1.455
61.798
 93 A; 84
 /product= "BASB059"
 /*tag=
 Location/Qualifiers
 339 BP
 from:
 Ç
 Length:
Gaps:
Percent Identity:
 84 G;
 _
 <u>.</u>
 78 T; 0 other;
 invasive
 : 89
: 1
: 29.213
 bacterial disease;
 is useful
 109
 40
 diagnostic
 for
```

alignment\_scores:

Quality: Ratio:

80.00 1.455 61.798

Percent

Length: Gaps: Identity:

1 29.213

Percent Similarity:

```
seq_documentation_block:
ID AAA15300 standard;
 seq_name:
 The present sequence encodes a protein that is specific for pathogenic strains of Neisseria. The polynucleotides, polypeptides, or their antigenic fragments, are used in vaccines to treat or protect against Neisseria infections, particularly by N. meningitidis. The polynucleotide sequence is also used for recombinant production of the polypeptide and to produce attenuated Neisseria strains that
 CDS
Sequence 339 BP; 93 A; 84 C;
 Claim 2; Page 69; 187pp; French.
 overexpress
 New polypeptide specific or preventative vaccines
 Aujame L,
Tinsley C,
 (INMR) PASTEUR MERIEUX SERUMS & VACCINS SA. (INRM) INSERM INST NAT SANTE & RECH MEDICALE
 30-OCT-1998;
 28-OCT-1999;
 11-MAY-2000.
 Neisseria
 04-SEP-2000
 AAA15300;
 260
 160
 WO200026375-A2
 Pathogenic
 DNA encoding a polypeptide of
 210 CCAATGCTATGTTACCAGTGTAATCAGCACAATCGGCGTTACCACTTCCG
 90
 40
 isThrAlaIleLeuAlaProAsnArgTrpGlnGluIleLeuSerLeuIle
 ATGCAATTTGTTTGG
 IleSerPheLeuTrp
 AATGAAAGCATACGCATCAACTTTACCGCAACTGTGGGTAAGCGCGTGAG
 GlySerAlaAspSerIleSerPheMetIleValVal.IleLysPheGlyH
 lnThrIleIleLysGlyLysThrAsnLysGlnGluIleSerSerArgPhe
 CGTTTGCCTTGGGCGTCAGCCAAAATGCCGTAAAAATCAGCAACCGCAGC
 2000-365622/31.
DB; AAY93269.
 /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:AAA15300
 meningitidis
 Bouchardon Perrin A;
 strain; Neisseria;
 (first entry)
 98FR-0013693
 99WO-FR02643
 or express it in a non-toxic mutant form.
 Location/Qualifiers
 DNA;
 274
 94
 P,
 339
 for
and
 Renauld-Mongenie G,
 ВP
84 G; 78 T; 0 other;
 pathogenic Neisseria useful for diagnosis -
 vaccine;
 a Neisseria pathogenic strain.
 Neisseria infection; ss.
 Rokb1
 В,
 89
 209
 159
 in
 Nassif
 therapeutic
```

alignment\_block: US-10-048-197-2 x AAA15300

Align seg 1/1 to: AAA15300

. 6

```
seq_documentation_block:
ID AAA05521 standard; DNA; 900 BP.
 seq_name: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2000.DAT:AAA05521
AAV81501 to AAV81679 represent specifically claimed protein sequences isolated from Streptococcus pneumoniae. AAA05407 to AAA05590 represent specifically claimed nucleotide sequences isolated from S. pneumoniae. The sequences have antibacterial and antiinflammatory properties. The protein sequences, and fragments of them, are useful as immunogens
 260
 210
 160
 110
 Gilbert CFG,
 Streptococcus pneumoniae.
 Streptococcus pneumoniae; vaccine; screening; protein antigen; antibacterial; antiinflammatory; meningitis; infection; diagnosis;
 Streptococcus
 24-MAY-2000
 Claim 7;
 New Streptococcal protein, useful as a vaccine, pneumococcal diseases and for screening agents or inhibiting expression of the protein
 WPI; 2000-195300/17.
 27-JUL-1998;
19-MAR-1999;
 27-JUL-1999;
 10-FEB-2000.
 WO200006737-A2
 pneumococcal disease; ds.
 (MICR-) MICROBIAL TECHNICS
 57
 90
 73
 6
 60
 23
 10
 CTCAATCAATGTAACCGTTTCCGACCAGAAACTTCAGGAACGTGCCG 109
 GCATCATCGCTTCGCCTCGTTGCGTTGCCATTAGCAGGTTGCGG 59
 ATGCAATTTGTTTGG 274
 IleSerPheLeuTrp 94
 isThrAlaIleLeuAlaProAsnArgTrpGlnGluIleLeuSerLeuIle
 AATGAAAGCATACGCATCAACTTTACCGCAACTGTGGGTAAGCGCGTGAG
 CGTTTGCCTTGGGCGTCAGCCAAAATGCCGTAAAAATCAGCAACCGCAGC 159
 CCAATGCTATGTTACCAGTGTAATCAGCACAATCGGCGTTACCACTTCCG 259
 GlySerAlaAspSerIleSerPheMetIleValVal.IleLysPheGlyH 73
 InThrIleIleLysGlyLysThrAsnLysGlnGluIleSerSerArgPhe 56
 lSerThrGlyAsnValAlaMetLysGluGlnAsnGlnGlnThrIleGluG
 ArgLeuThrIleSerAlaLeuLeuThrAlaLeuLeuValThrGlyCysVa
 Page 54; 108pp; English.
 (first entry)
 pneumoniae type 4 nucleotide sequence 4170.6.
 Hansbro
 98GB-0016337.
99US-0125164.
 99WO-GB02451
 PM
 CID
 , for diagnosis of capable of antagonizing
 40
 89
 209
 23
```

```
seq_documentation_block:
ID AAV52208 standard; DN
XX
AC AAV52208;
XX
DT 23-OCT-1998 (first e
XX
Streptococcus pneumon
XX
KW Streptococcus pneumon
XX
Computer readable mec
XX
Streptococcus pneumon
XX
WO9818931-A2.
XX
PN WO9818931-A2.
XX
PD 07-MAY-1998.
 88888888888
 alignment_scores:
Quality:
 us-10-048-197-2 x AAA05521
 seq_name:
 Align seg 1/1 to: AAA05521
 Percent Similarity:
 and/or antigens. The nucleotide sequences can be used in vaccines and in diagnostic assays. The proteins and nucleotides can be useful for the detection and diagnosts of S. pneumoniae. The protein sequences are also useful for screening an agent capable of antagonising, inhibiting or interfering with the function or expression of the proteins in which the agent is useful for treatment or prophylaxis of S. pneumoniae infection and meningitis. AAAO5591 to AAAO5504 represent primers used in the
 567
 520
 482
 382
 332
 Streptococcus pneumoniae; S. pneumoniae; genome; diagnosis; computer readable medium; vaccine; pharmaceutical compositions of the composition of t
 100
 282
 232 CTAGGAGCCTTGGTAACAGCTGTGATTCTCGTAACGGGCTCTGTTCTAGT
 Sequence 900 BP;
 exemplification of the present invention.
 Streptococcus pneumoniae genome
 84
 67
 44
 25 r.....GlyAsnValAlaMetLysGluGlnAsnGlnGlnThrIleGluG
 10 IleSerAlaLeuLeuThrAla...LeuLeuValThrGlyCysValSerTh
 oLysAsnLeuSerPheTyrLeuThrAlaLys 110
 GluIleLeuSerLeuIleIleSerPheLeuTrpValLysProTyrArgPr 100
 TTGTTCTTCGATTTACGGACTGGTATATCCTAGATCCT......
 alValIleLysPheGlyHisThrAlaIleLeuAlaProAsnArgTrpGln
 GCATTTTCTGGAAGATACGCTAGGGTGGGTAGCTGTTATCCTGATGGCGA 481
 AGTCTGGTGGTTAGGTAAGGGAAAGACAAAGAATGAGTCTATTCTGAGTCT 431
 lnThrIleIle.....
 CATTTTGGAAAATGTCACGAAGATTTTGCATCCGCAACCAGTCAATGATG
 ...CTTTTGTCCCTTGTCATTTCTTTCTTTATTCTTTCAAAAGCCCCTTCC
 AGGGGATTCTCTGGTTAGGAATTATTGCGATTACTATCAATCTGTTAGCG
 ACGT.....TTTTGGTCTACACTCAAG
 LysGlyLysThrAsnLysGlnGluIleSerSerAr
 /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:AAV52208
 Ratio:
 (first entry)
 pneumoniae
 78.00
1.200
51.181
 240 A; 155 C;
 DNA;
 8136
 from: 1
 Percent
 ΒP
 211 G; 294 T; 0 other;
 fragment SEQ
 ç
o:
 Identity:
 pharmaceutical composition;
 900
 IJ
 127
 NO:75
 566
 519
 381
 43
 40
 25
 in which the
 also
```

```
alignment_block:
US-10-048-197-2 x AAV52208
 alignment_scores:
 Streptococcus pneumoniae. The present invention also describes an CC isolated nucleic acid molecule encoding a homologue of any of the CC fragments of the S.pneumoniae genome (SEQ ID NO:1 to 391) where the CC nucleic acid molecule is produced by a process comprising: (a) screening CC a genomic DNA library using as a probe a target sequence defined by any CC of the sequences in SEQ ID NO:1 to 391, identifying members of the CI library which contain sequences that hybridise to the target sequence and isolating the nucleic acid molecules from the members; or (b) isolating CC mRNA, DNA or cDNA produced from an organism, amplifying nucleic acid molecules whose nucleotide sequence is homologous to amplification or cDNA produced from an organism, amplifying nucleic acid conclecules whose nucleotide sequence is homologous to amplification or primers derived from the fragment of the S. pneumoniae genome to prime the amplification and isolating the amplified sequences. The computer creadable medium can be used in a computer-based system for identifying CC fragments of the S. pneumoniae genome. Products from the present invention can be used in diagnosis kits and assays, and CC pharmaceutical compositions and vaccines for S. pneumoniae.
 Align seg 1/1 to: AAV52208
 Percent Similarity:
 2026
 1976
 2076 AGTCTGGTGGTTGGTAAGGGAAAGACAAAGAATGAGTCTATTCTGAGTCT
 1926 CTAGGAGCCTTGGTAACAGCTGTGATTCTCGTAACGGGCTCTGTTCTAGT
 Computer-readable medium with recorded Streptococcus pneumoniae polynucleotide sequences - useful in diagnostic kits and assays, pharmaceutical compositions and vaccines for Streptococcus
 Sequence 8136 BP;
 pharmaceutical compositions and vaccines for S. pneumoniae.
 the nucleotide sequences SEQ ID NO:1 to 391 (AAV52134 to AAV52524) recorded on it, or a representative fragment or a sequence at least identical to SEQ ID NO: 1 to 391. The nucleotide sequences depicted SEQ ID NO:1 to 391 (AAV52134 to AAV52524) are genomic fragments from
 44
 Claim
 pneumoniae
 (HUMA-) HUMAN GENOME SCI INC
 31-OCT-1996;
 30-OCT-1997;
 55
 40
 25
 10 IleSerAlaLeuLeuThrAla...LeuLeuValThrGlyCysValSerTh ::::::|||||||| ||| ::
gPheGlySerAlaAspSerIleSerPhe...
 CATTTTGGAAAATGTCACGAAGATTTTGCATCCGCAACCAGTCAATGATG
 AGGGGATTCTCTGGTTAGGAATTATTGCGATTACTATCAATCTGTTAGCG
 InThrIleIle.....
 r.....GlyAsnValAlaMetLysGluGlnAsnGlnGlnThrIleGluG
 present invention describes a computer readable medium which has
 1;
 Quality:
 Page
 Ratio:
 Rosen CA;
 Choi GH,
 617-622;
 96US-0029960
 97WO-US19588
 ...LysGlyLysThrAsnLysGlnGluIleSerSerAr 55
 78.00
1.200
51.181
 2249
 Dillon PJ,
 A; 1481 C; 1983 G; 2423 T; 0 other;
 1409pp; English.
 from: 1
 Percent
 ;
;
 Identity:
 Dougherty BA,
 Length:
 28
 Fannon
 1975
 2075
 2025
 43
 40
 and
 'n
```

```
seq_documentation_block:
ID AAS62620 standard; cDNA;
 seq_name:
 2261
 2176
 2214
 2126 GCATTTTCTGGAAGATACGCTAGGGTGGGTAGCTGTTATCCTGATGGCGA 2175
 which encode human secreted proteins. The CDNA sequences have been derived from a variety of human tissues. The invention also provides a method for producing proteins from these polynucleotide sequences. The proteins are useful for identifying compounds that modulate their activity and production, and the cell is also useful for identifying compounds that modulate expression of the polynucleotide sequences encoding the secreted proteins. The sequences of the invention are useful for treating diseases such as hyperproliferative disorders (e.g. cancer), immune deficiency disorders (e.g. severe combined
 immunodeficiency (SCID)), autoimmune disorders (e.g. multiple sclerosis), blood disorders (e.g. thrombocytopaenia), inflammatory disorders (e.g. arthritis) and infectious disorders (e.g. hepatitis) The polynucleotide sequences of the invention are also useful in get therapy. AAS62214-AAS62838 represent the CDNA sequences of the invention that encode for novel human secreted proteins.
 New polynucleotides encoding secreted proteins useful for treating e.g. asthma, {\sf HIV} and {\sf Crohn's} disease -
 WPI;
 06-APR-2000;
 29-MAR-2001; 2001WO-US10485
 cDNA sequence #407 encoding novel human secreted
 100
 Claim 1; Page 289-290; 391pp; English.
 Gulukota K,
 Wong GG,
 WO200177291-A2
 Homo sapiens.
 Human secreted
 14-FEB-2002
 (GEMY) GENETICS INST INC.
 18-OCT-2001
 infectious disorder; gene therapy; antimicrobial; hepatotropic;
 84
 67
 mmune deficiency
 ACGT.....TTTTGGTCTACACTCAAG 2282
 GluIleLeuSerLeuIleIleSerPheLeuTrpValLysProTyrArgPr :::|||||||||||||::: :::::: ||
 present invention
 TTGTTCTTCGATTTACGGACTGGTATATCCTAGATCCT
 alValIleLysPheGlyHisThrAlaIleLeuAlaProAsnArgTrpGln
 oLysAsnLeuSerPheTyrLeuThrAlaLys 110
 ... CTTTTGTCCCTTGTCATTTCTTTCTTTATTCTTTCAAAAGCCCCTTCC
 2002-010900/01.
 /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:AAS62620
 Clark HF,
 Graham JR;
 2000US-195604P.
 (first entry)
 protein; hyperproliferative disorder; autoimmune disorder;
ncy disorder; blood disorder; inflammatory disorder;
 disorder;
 Fechtel K,
 relates to the isolation
 1709
 ΒP
 Agostino MJ,
 of novel cDNA sequences
 Howes
 protein.
 (e.g. hepatitis).
 SH,
 2260
 100
 2213
 83
 Resnick RJ;
 in gene
```

alignment\_scores:

Sequence 1709

BP;

481

A,

358

Ç

421 G;

449 Τ;

0 other;

```
alignment_block:
US-10-048-197-2 x AAS62620
 seq_documentation_block:
ID AAF28550 standard; DNA; 99629 BP
 seq_name: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:AAF28550
 Align seg 1/1 to: AAS62620
 Ratio:
Percent Similarity:
 574
 524
 474
 424
 374
 324 TATCAAAAACATGATTACAGGGACATCTCAGGCTGACTGTGCTGTCCTGA 373
 274
 224
 Genomic library; bacteria; human upper airway; otitis media; sinusitis; bronchopulmonary; endocarditis; meningitis; ss.
 Genomic fragment #37.
Genomic library for identifying diagnostic and therapeutic compositions, and for identifying virulence factors, reguli
 WPI; 2001-041427/05
 16-JUN-2000;
 28-DEC-2000
 WO200078968-A2
 Moraxella catarrhalis.
 04-APR-2001 (first entry)
 AAF28550;
 (INCY-) INCYTE GENOMICS INC.
 18-JUN-1999;
 57
 67
 47
 23
 97
 80
 38
 10 IleSerAlaLeuLeuThrAlaLeuLeuValThrGlyCys......
 nArgTrpGlnGluIleLeuSerLeuIleIleSerPheLeuTrpValLysP 97
 AATTGTCGGTGTTAACAAAATGGATTCACTGAGCCACCCTACAGCCAGAA 523
 CAGACCCGAGAGCATGCCCTTCTGGCTTACACACTGGGTGTGAAACAACT 473
 TTGTTGCTGCTGGTGTTGGTGAATTTGAAGCTGGTATCTCCAAGAATGGG 42:
 ACCAGCAAGTACTATGTGACTATCATTGATGCCCCAGGACACAGAGACTT 32:
 ValSerThrGlyAsnValAlaMetLysGluGlnAsnGlnGlnThrI 38
 GCTACAACCCCGACACAGTAGCATTT
 roTyrArgProLysAsnLeuSerPhe 105
 GAGATATGAGGAAATTGTTAAGGAAGTCAGCACTTACATTAAGAAAATTG 57:
 ValValIleLysPheGlyHisThrAlaIleLeuAlaPro.As 80
 ThrAsnLysGlnGluIleSerSerArgPheGl 57
 leGluGlnThrIleIleLysGlyLys......46
 CTGAGCGTGAACGTGGTATCACCATTGATATCTCCTTGTGGAAATTTGAG
 RE,
 Quality:
 Patterson
 2000WO-US16649.
 99US-0140121
 74.50
1.112
53.175
 Ç
 from:
 Berg
 Percent
 599
 2
 Identity:
 to: 1709
 21.429
regulatory
 273
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```
seq_documentation_block:
ID ABL10149 standard; cE
XX
AC ABL10149;
XX
DT 26-MAR-2002 (first e
XX
DT Drosophila melanogast
XX
KW Drosophila; developme
KW pharmaceutical; gene;
XX
OS Drosophila melanogast
XX
XX
OS Drosophila melanogast
 alignment_scores:
Quality:
Ratio:
 SXCCCCCCCCCXPX PF
 alignment_block:
US-10-048-197-2 x AAF28550/rev
 seq_name: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:ABL10149
 Align seg 1/1 to reverse of: AAF28550
 Percent Similarity:
 76540
 76558
 76708 TATCAAATTTCCACGACCCTGAACTCACTCCTTCAGGCAGTGTCAATGAT 76659
 76608
 76658 AAGCGTTCTTGATACACATAATGCTTCGGTGTAACAACAAAATTCACTAC 76609
 76453 AAGCCATAGAATAAATCCAATTTTTTA 76427
 76500 TGGTAAGGCTACGCCAACTGATACCGCACCGACAATGGATACGCCCA...
 The present invention relates to a Moraxella catarrhalis genomic library comprising of a combination of 41 nucleic acid molecules (see AAF28514-AAF28534). The library has a number of uses described in the specification e.g. is useful for aidentifying diagnostic and therapeutic compositions. M. catarrhalis (Branhamella catarrhalis) is a large
 acids
 elements and drug targets, comprises Moraxella catarrhalis nucleic
 Claim 1;
 Drosophila; developmer
pharmaceutical; gene;
 Sequence 99629 BP;
 and meningitis.
 Drosophila melanogaster
 Drosophila melanogaster expressed polynucleotide
 ABL10149 standard; cDNA;
 aerobic, gram-negative diplococcus, normally found among the bacterial flora of human upper airways. M. catarrhalis is known to cause acute, localised infections such as otitis media, sinusitis and bronchopulmonary infection and life-threatening, systemic diseases including endocarditis
 85
 8
 52
 37
 20
 99 ArgProLysAsnLeuSerPheTyrLeu
 4 HisHisIleArgLeuThrIleSerAlaLeuLeuThrAlaLeuLeuValTh
 GCAAAAACTTTGGCTGGC......
 hrIleGluGlnThrIle.....IleLysGlyLysThrAsnLysGlnGlu 51
 AAGTTCATCACCCACTTGAGATGATGAAACCTTAAACGCTTCATGAACAG
 rGlyCysValSerThrGlyAsnValAlaMetLysGluGlnAsnGlnGlnT 37
 leLeu.....SerLeuIleIleSerPheLeuTrpValLysProTyr
 IleSerSerArgPheGlySerAlaAspSerIleSerPheMetIleValVa 68
 TGGTATCCCCAAATAGCGATGCCAAACCATTGGCAGACGC 76501
 lIleLysPheGlyHisThrAlaIleLeuAlaProAsnArgTrpGlnGluI
 Page 391-415;
 developmental biology;
 (first entry)
 71.00
1.224
53.211
 29233 A; 19222 C; 21909 G;
 ss.
 545pp; English
 969
 Percent
 Gaps:
Identity:
 cell signalling;
 from: 1
 22.936
 to: 99629
 29264 T; 1 other;
 SEQ
 ä
 85
 76559
 NO 24929
```

```
seq_documentation_block:
ID ABL10148 standard; cD
XX
AC ABL10148;
XX
DT 26-MAR-2002 (first e
XX
DE Drosophila melanogast
XX
KW Drosophila; developme
KW pharmaceutical; gene;
XX
 seq_name: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:ABL10148
 alignment_block:
US-10-048-197-2 x ABL10149/rev
 alignment_scores
 Align seg 1/1 to reverse of: ABL10149
 Percent Similarity:
 pharmaceutical; gene;
 Drosophila; developmental biology; cell signalling;
 797
 832
 capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
 Sequence 969 BP; 271 A;
 Claim 1; SEQ ID NO 24929; 21pp + Sequence Listing; English.
 The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from
 The invention relates to an isolated nucleic acid detection
 New isolated nucleic acid
genes from Drosophila and
interactions -
 23-MAR-2000;
11-JUL-2000;
 98
 Venter JC,
 (PEKE) PE CORP NY.
 23-MAR-2001;
 70 sPheGlyHis...ThralalleLeualaProAsnArgTrpGlnGluIleL 86
 interactions
 WO200171042-A2
 ABB57737-ABB72072)
 ftp.wipo.int/pub/published_pct_sequences.
 TTTCGGCCACTTCGAAGCCATCCTTGCGCCC
 SerArgPheGlySerAlaAspSerIleSerPheMetIleValValIleLy 70
 CATCTATCGTAATCGCATTTCTG 775
 euSerLeuIleIleSerPheLeu
 2001-656860/75
 Quality:
Ratio:
 melanogaster expressed polynucleotide SEQ
 Adams M,
 (first entry)
 2000US-191637P
2000US-0614150
 2001WO-US09231
 70.00
2.500
68.293
 cDNA; 2969
 SS.
 Ŀ
 228 C;
 , DWG
 Percent
 detection reagent for detecting 1000 or more for elucidating cell signalling and cell-cell
 93
 ВP
 249 G;
 Myers
 Identity:
 from:
 Length:
Gaps:
 EW;
 221 T; 0 other;
 Ь
 41
2
43.902
 ;
6
 969
 ID NO
 WIPO
 is
```

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XX D XX D XX XX
 alignment_block:
US-10-048-197-2 x ABL10148/rev
 seq_name: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:ABL12634
 alignment_scores:
 Align seg 1/1 to reverse of: ABL10148
 Percent Similarity:
 1832 TTTCGGCCACTTCGAAGCCATCCTTGCGCCC
 1797 CATCTATCGTAATCGCATTTCTG
 Drosophila;
 Drosophila melanogaster expressed polynucleotide SEQ ID NO 32384
 26-MAR-2002
 ABL12634 standard;
 ABL12634;
 The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating call signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLIGIT6-ABLIGOT1), expressed DNA sequences (ABLIGIT6-ABLIGOT1), expressed DNA sequences (ABLIGIT6-ABLIGOT1).
 Sequence 2969 BP; 878 A;
 Claim 1; SEQ ID NO 24926; 21pp + Sequence Listing; English
 genes from Drosophila and interactions -
 New isolated nucleic acid
 (PEKE) PE CORP NY.
 23-MAR-2000;
11-JUL-2000;
 23-MAR-2001;
 27-SEP-2001
 70 sPheGlyHis...ThrAlaIleLeuAlaProAsnArgTrpGlnGluIleL 86
 The sequence data for this patent did not form specification, but was obtained in electronic in
 WO200171042-A2
 Drosophila melanogaster.
 54 SerArgPheGlySerAlaAspSerIleSerPheMetIleValValIleLy
 ABB57737-ABB72072)
 ftp.wipo.int/pub/published_pct_sequences.
 euSerLeuIleIleSerPheLeu
 2001-656860/75.
DB; ABB66045.
 Quality:
 ر
ر
 Ratio:
developmental biology; cell signalling;
 Adams
 (first
 2000US-191637P.
2000US-0614150.
 2001WO-US09231
 but was obtained in electronic
 70.00
2.500
68.293
 ź
 cDNA;
 entry)
 3319
 613 C; 618 G; 860 T; 0
 PWD,
 Gaps:
Percent Identity:
 detection reagent for detecting 1000 or more for elucidating cell signalling and cell-cel
 1775
 93
 Myers
 from: 1
 ¥
 41
2
43.902
 ;
:
 n part of the printed format directly from
 ATCA 1798
 insecticide;
 and cell-cell
 WIPO
```

żs

```
seq_documentation_block:
ID AAX13387 standard; DNA; 4
XX
AC AAX13387;
XX
DT 19-MAR-1999 (first entry
XX
DE Enterococcus faecalis gen
 alignment_block:
US-10-048-197-2 x ABL12634/rev
 alignment_scores:
 seq_name: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1999.DAT:AAX13387
 Align seg 1/1 to reverse of: ABL12634
 Percent Similarity:
 The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The inventuseful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
 520
 570
 The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from at ftp.wipo.int/pub/published_pct_sequences.
 23-MAR-2000;
11-JUL-2000;
 W0200171042-A2
 Enterococcus faecalis genome contig SEQ ID NO:450.
 Claim 1; SEQ ID NO 32384; 21pp + Sequence Listing; English
 New isolated nucleic acid
genes from Drosophila and
interactions -
 23-MAR-2001; 2001WO-US09231.
 27-SEP-2001
 Drosophila melanogaster
 pharmaceutical; gene;
 Sequence 3319 BP;
 Venter JC,
 (PEKE) PE CORP NY
 70 sPheGlyHis...ThrAlaIleLeuAlaProAsnArgTrpGlnGluIleL 86
 54 SerArgPheGlySerAlaAspSerIleSerPheMetIleValValIleLy 70
 euSerLeuIleIleSerPheLeu 93
 TTTCGGCCACTTCGAAGCCATCCTTGCGCCC
 2001-656860/75
 Quality:
Ratio:
 ABB68531.
 Adams M,
 2000US-191637P
2000US-0614150
 (first entry)
 70.00
2.500
68.293
 928 A; 721 C;
 88
 E
 4239
 PWD,
 Length: 41
Gaps: 2
Percent Identity: 43.902
 detection reagent for detecting 1000 or more for elucidating cell signalling and cell-cel
 463
 ВР
 Myers
 758 G;
 from:
 EΨ
 912 T; 0 other;
 ب
 to: 3319
 ATCA 486
 format directly from
 The invention
 cell-cell
 and
 WIPO
 SŢ
```

```
alignment_block:
US-10-048-197-2 x AAX13387
 alignment_scores:
 Align seg 1/1
 Percent Similarity:
 14-NOV-1997;
06-MAY-1997;
16-MAY-1997;
 A computer readable medium has been developed which has recorded on it 982 nucleotide sequences isolated from the Enterococcus faecalis genome. AAX12938 to AAX13919 represent these nucleotide sequences which are primary nucleotide sequences, also known as contigs. The computer-based system can identify fragments of the Enterococcus faecalis genome with commercial importance. The products see used to detect the presence of Enterococcus faecalis in samples. They can also be used for diagnosing Enterococcal infection in an animal and monitoring progression of disease, and for identifying agents which can be used to modulate the growth or pathogenicity of Enterococcus faecalis, or another related organism, in vivo or in vitro. In particular the polypeptides encoded by the Enterococcus faecalis nucleotide sequences
 New isolated Enterococcus faecalis polynucleotides and polypeptides - used to develop products for the detection of Enterococcus and for use in vaccines for prevention or attenuation of Enterococcus
 963 TTCAATTATTAATTCGGGGTATTTTCTAAAGTGGAACAACGTCAAGTAT 1012
 Sequence 4239
 can be used in vaccines to prevent or attenuate an Enterococcal
 Claim 1; Page 1681-1683; 2084pp; English
 Barash
 04-MAY-1998;
 Enterococcus
 Enterococcus faecalis; contig; detection; Enterococcal infection; vaccine; attenuation; computer readable medium; ds.
 WPI; 1999-045171/04.
 (HUMA-) HUMAN GENOME SCI INC.
 12-NOV-1998
 WO9850555-A2
 54
 37
 intection.
 20
 6 IleArgLeuThrIleSerAla.....LeuLeuThrAlaLeuLeuValTh
 SerArgPheGly...SerAlaAspSerIleSerPheMetIleValValIl 69
 hrIleGluGlnThrIleIleLysGlyLysThrAsnLysGlnGluIleSer 53
 rGlyCysValSerThrGlyAsnValAlaMetLysGluGlnAsnGlnGlnT
AGTWSTGAYGGYAAAACAARAGAAAAAATCAAGTTTCCAAAAATTTATTA 1112
 Quality:
Ratio:
 S
 8
 Dillon PJ,
 faecalis
 BP;
 97US-0066009.
97US-0044031.
97US-0046655.
 AAX13387
 98WO-US08985
 70.00
1.148
63.542
 1556
 Ą.
 Kunsch CA;
 from: 1
 477
 Percent
 Ç;
 901 G;
 Gaps:
Identity:
 to: 4239
 Length:
 1292
 96
3
26.042
 Ŧ.
 13 other;
 1062
 37
 962
 20
```

```
alignment_block:
 alignment_scores
 seq_documentation_block:
ID AAF28552 standard;
 Align seg 1/1 to:
 US-10-048-197-2 x AAF28552
 Percent Similarity:
 seq_name: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:AAF28552
50328 ATAATGATGAGATTTTATTGGTTGGATGCTTGGCAACCTTATTTTACT 50377
 The present invention relates to a Moraxella catarrhalis genomic library comprising of a combination of 41 nucleic acid molecules (see AAF28514-AAF28554). The library has a number of uses described in the specification e.g. is useful for aidentifying diagnostic and therapeutic compositions. M. catarrhalis (Branhamella catarrhalis) is a large aerobic, gram-negative diplococcus, normally found among the bacterial flora of human upper airways. M. catarrhalis is known to cause acute, localised infections such as otitis media, sinusitis and bronchopulmonary infection and life-threatening, systemic diseases including endocarditis
 1113
 1163
 Sequence 100848
 and meningitis.
 Claim 1; Page 436-459; 545pp; English.
 Genomic library for identifying diagnostic and therapeutic compositions, and for identifying virulence factors, regulatory compositions and drug targets, comprises Moraxella catarrhalis nucleic
 WPI; 2001-041427/05
 WO200078968-A2
 Genomic library; bacteria; human upper airway; otitis media; sinusitis; bronchopulmonary; endocarditis; meningitis; ss.
 04-APR-2001 (first entry)
 Lagace RE,
 (INCY-) INCYTE GENOMICS INC.
 18-JUN-1999;
 16-JUN-2000; 2000WO-US16649.
 Moraxella catarrhalis
 Genomic fragment #39
 AAF28552;
 28-DEC-2000
 81
 69
 LeuLeuThrAlaLeuLeuValThrGlyCysValSerThr......
 AATTTCAGGAAAATTTGAAACCATTGGTGGCTTTTTG 1200
 TAAGTCTGCAAAAATAGTATTTTYGTTTCATTTGAAACAGCRGGTAATA 1162
 eLysPheGlyHisThrAlaIleLeu.....AlaProAsnA
 rgTrpGlnGluIleLeuSerLeuIleIleSerPheLeu
 Quality:
Ratio:
 Patterson C, Berg KL;
 AAF28552
 99US-0140121
 B₽;
 70.00
0.986
 46.405
 DNA; 100848 BP
 28518
 from:
 Α;
 Percent Identity:
 19877
 ᆫ
 .
6
 C; 22976 G;
 Length:
Gaps:
 100848
 153
10
27.451
 93
 29477 T; 0 other;
 81
```

```
seq_documentation_block:
ID AAF55109 standard;
 seq_name: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:AAF55109
 50769 CAAGGCT 50775
 50722 ATACAGGTTATTCCAAGGCGGATGAAGTGTTTGAATTTT...ATCACAAT 50768
 50628 GAAA.....CATTAGATGTTACTCTGCCCGTGGGAAGTTATGTCGTGAA 50671
 50578
 50528 TTTACAAATAAAAACCAACTCAGGAAGTCATTATTGGGTAAAAATTGTCA 50577
 50428
 50378
WPI; 2001-159873/16.
P-PSDB; AAB67488.
 Thonnard
 31-лиц-2000;
 08-FEB-2001.
 WO200109336-A1
 BASB119; immune response; bacterial infection; generatitis media; pneumonia; sinusitis; nosocomial infection; invasive disease; hearing loss; fluid accumulation;
 Nucleotide sequence of a BASB119 polypeptide.
 109 aLysAla 111
 (SMIK) SMITHKLINE BEECHAM BIOLOGICALS
 Moraxella catarrhalis
 15-MAY-2001 (first entry)
 AAF55109;
 93 LeuTrpValLysProTyrArgProLysAsnLeuSerPheTyrLeuThrAl 109
 69
 59
 45
 40
 26
 snArgTrpGlnGluIleLeu.....SerLeuIleIleSerPhe 92
 eLysPheGlyHisThrAlaIleLeuAlaPro...... 80
 ATGCTTATGACGAGCGAGAAGAGCTGGTGAGTTATTTTATCCGTGGTGGA 50627
 TTGCCAGAGACAGGGGCAACCAACAAACCTAATTTGTATGGCGATTCACC 50527
 AATCAAGCCCAAGAATTACAATAAAAAATGAATGATCGAAGCTCAACCG
 lnThr.......IleIleLys........
 TGGGTGTGGTAATAATTCTAGTCAAGAATTAGAGACGAATACCATTGAAC
 GlyLysThrAsnLysGln...
 GluïleSerSerArgPheGlySer............
 GlyAsnValAlaMetLysGluGlnAsnGlnGlnThrIleGluG
 2000WO-EP07363
 99GB-0018302.
 /*tag= a
/product=
 Location/Qualifiers
1..513
 'note= "no termination
 DNA; 513 BP
 "BASB119"
 codon given"
 genetic immunization;
infection;
 antibacterial;
 50427
 50
 44
 50477
 40
```

```
alignment_block:
 are useful for generating an immune response in an animal. The polypeptides may also be used as prophylactic agents of bacterial confections, particularly M. catarrhalis infections in mammals, caterials in fections in mammals, caterials in a section against these infections or diseases. These diseases include otitis media in infants or children, pneumonia in elderlies, sinusitis, nosocomial infections and invasive diseases, chronic otitis media with hearing loss, fluid cancumulation in the middle ear, infection of the upper respiratory tract, or inflammation of the middle ear. The polypeptides or polynucleotides may also be employed as research reagents and materials cf of discovering treatments of and diagnostics for diseases, caterials compounds, or for discovery and development of the antibacterial compounds, or or for disgnostics staging of the caterials can be accorded to the caterials can be caused as a second of the caterials can be caterials.
 US-10-048-197-2 x AAF55109
 Align seg 1/1 to: AAF55109
 Percent Similarity:
 245
 295
 Sequence 513
 The present sequence encodes a BASB119 polypeptide of Moraxella catarrhalis strain ATCC43617. BASB119 polypeptides and polynuclo
 Claim 13;
 New BASB119 polypeptides and polynucleotides from Moraxella catarrhalis strain ATCC 43617, useful as therapeutic agents or vaccines against bacterial infections, e.g. otitis media or pneumonia -
 195
 51
 $
 95
 39
 54
 22 sValSerThrGlyAsnValAlaMetLysGluGlnAsnGlnGlnThrIleG
 4
 6 IleArgLeuThrIleSerAlaLeuLeuThrAlaLeuLeuValThrGlyCy
lIleLysPheGlyHisThrAlaIleLeuAlaPro.....
 TCAATGCTTATGACGAGCGAGAAGAGCTGGTGAGTTATTTTATCCGTGGT
 GGAGAAA.....CATTAGATGTTACTCTGCCCGTGGGAAGTTATGTCGT
 ACCTTTACAAATAAAAACCAACTCAGGAAGTCATTATTGGGTAAAAATTG
 CCGTTGCCAGAGACAGGGGCAACCAACAAACCTAATTTGTATGGCGATTC 194
 luGlnThr......IleIleLys.....
 T.....GGTAATAATTCTAGTCAAGAATTAGAGACGAATACCATTG
 ATGAGATTTTTATTGGTTGGATGCTTGGCAACCTTATTTTTACTTGGGTG
 GluIleSerSerArgPheGlySer.........
 AACAATCAAGCCCAAGAATTACAATAAAAATGAAATGATCGAAGCTCAA 14
 GlyLysThrAsnLysGln.......
 AsnArgTrpGlnGluIleLeu.....SerLeuIleIleSer
 Quality:
 determining the response of an infectious organism to drugs.
 Ratio:
 Page 65; 83pp; English
 BP; 173 A;
 69.50
0.952
47.403
 78 C;
 from: 1
 Length:
Gaps:
Percent Identity:
 111 G;
 .
6
 151 T;
 513
 154
10
27.922
 0 other;
 91
 338
 294
 89
 244
 50
 44
 94
 39
 53
 polynucleotides
 79
 58
```

```
seq_name: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:AAF55108
 cc are useful for generating an immune response in an animal. The polypeptides may also be used as prophylactic agents of bacterial confections, particularly M. catarrhalis infections in mammals, caspect ally humans. The polynucleotides are useful in therapy or prophylaxis, particularly genetic immunization against these infections or diseases. These diseases include otitis media in infants or confideren, pneumonia in edderlies, sinusitis, nosocomial infections and cinvasive diseases, chronic otitis media with hearing loss, fluid cacumulation in the middle ear. The polypeptides or tract, or inflammation of the middle ear. The polypeptides or polynucleotides may also be employed as research reagents and materials conforting treatments of and diagnostics for diseases, plant of the confideration of the diseases. In particular, the polypeptides or colynucleotides are useful in the discovery and development of the categories of the confideration of the categories of the cate
 New BASB119 polypeptides and polynucleotides from Moraxella catarrhalis strain ATCC 43617, useful as therapeutic agents or vaccines against bacterial infections, e.g. otitis media or pneumonia -
 BASB119; immune response; bacterial infection; genetic immunization otitis media; pneumonia; sinusitis; nosocomial infection; invasive disease; hearing loss; fluid accumulation; antibacterial;
 436
 The present sequence encodes a BASB119 polypeptide of Moraxella catarrhalis strain ATCC43617. BASB119 polypeptides and polynucl
 Nucleotide sequence of a BASB119
 389 AAAATACAGGTTATTCCAAGGCGGATGAAGTGTTTGAATTTT...ATCAC
 (SMIK) SMITHKLINE BEECHAM BIOLOGICALS
 rAlaLysAla 111
 AATCAAGGCT
 445
 Location/Qualifiers
 the response of
 78 C;
 English.
 "BASB119"
 βP
 112 G;
 polypeptide.
 an infectious organism to
 152 T;
 0 other;
 genetic immunization;
infection;
 and polynucleotides
 drugs
 SS
```

alignment\_scores:

Quality:

69 . 50

```
seq_documentation_block:
ID AAC85071 standard; DN
XX
AC AAC85071;
XX
DT 08-MAY-2001 (first e
XX
DT 08-MAY-2001 (first e
XX
Atherosclerosis-assoc
X
 seq_name:
 alignment_block:
US-10-048-197-2 x AAF55108
 Align seg 1/1 to: AAF55108
 Ratio:
Percent Similarity:
 Atherosclerosis-associated gene; stroke; myocardial infarction; human; ischemia; coronary artery disease; angina pectoris; hypertension; peripheral vascular disease; renal artery stenosis; antiatherosclerotic; cerebroprotective; cardiant; gene therapy; hypotensive; vasotropic;
 28-JUN-2000; 2000WO-US17887
 Atherosclerosis-associated gene seq ID No.
 436
 389
 339
 295
 108 rAlaLysAla 111
 245
 195
 145 CCGTTGCCAGAGACAGGGGCAACCAAAACCTAATTTGTATGGCGATTC 194
 80
 8
 59
 51
 45
 95
 39 luGlnThr.....IleIleLys.....
 54
 22
 4 ATGAGATTTTTATTGGTTGGATGCTTGGCAACCTTATTTTACTTGGGTG
 AAAATACAGGTTATTCCAAGGCGGATGAAGTGTTTGAATTTT...ATCAC
 PheLeuTrpValLysProTyrArgProLysAsnLeuSerPheTyrLeuTh 108
 lIleLysPheGlyHisThrAlaIleLeuAlaPro.....
 TCAATGCTTATGACGAGCGAGAAGAGCTGGTGAGTTATTTTATCCGTGGT
 sValSerThrGlyAsnValAlaMetLysGluGlnAsnGlnGlnThrIleG 39
 AATCAAGGCT 445
 ..AsnArgTrpGlnGluIleLeu.....SerLeuIleIleSer
 GGAGAAA.....CATTAGATGTTACTCTGCCCGTGGGAAGTTATGTCGT
 ACCTTTACAAATAAAAACCAACTCAGGAAGTCATTATTGGGTAAAAATTG
 GluIleSerSerArgPheGlySer.........
 IleArgLeuThrIleSerAlaLeuLeuThrAlaLeuLeuValThrGlyCy
 /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:AAC85071
 ·····AlaAspSerIleSerPheMetIle.ValVa
 (first entry)
 GGTAATAATTCTAGTCAAGAATTAGAGACGAATACCATTG
 0.952
47.403
 DNA;
 868
 from:
 Gaps: 10
Percent Identity: 27.922
 ₽P
 ţo:
 7.
 435
 388
 91
 79
 294
 83
 244
 44
 58
 50
 94
 53
 22
seq_documentation_block:
ID AAC43179 standard; DN
XX
AC AAC43179;
XX
DT 17-OCT-2000 (first e
XX
DE Arabidopsis thaliana
XX
KW Hybridisation assay;
 alignment_block:
 alignment_scores:
 Align seg 1/1
 Percent Similarity:
 396
 346
 296
 84
 38
 Claim
 Jones KA,
 07-JUL-1999;
 Quality:
 Ratio:
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seq_name: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:AAC43179
 US-10-048-197-2 x AAC85071
Hybridisation assay; genetic mapping; gene expression control;
 Arabidopsis thaliana DNA fragment SEQ ID NO: 38318
 AAC43179 standard; DNA; 1014
 246 GACTTCACCAGTGGTCTTTGGCTTCATCAATTCACAGGAAATGGCATCAA
 196 TGTGTTTCCTACTCTTCTTTGTCTTGGAGGAAAGCAAAGGGAGAAATG
 useful in diagnosis, prognosis, treatment, prevention, selection and evaluation of therapies for atherosclerosis including stroke, myocardial infarction, transient cerebral ischemia, mesenteric ischemia, coronary artery disease, angina pectoris, peripheral vascular disease, renal artery stenosis, and hypertension. Sequences AAC85065-85098 represent atherosclerosis-associated genes of the invention.
 Sequence 868 BP; 249 A; 207 C; 182 G; 230 T; 0 other;
 The invention provides novel atherosclerosis-associated polynucleotides and polypeptides encoded by the genes. Expression vectors and host cells for producing the polypeptides are disclosed and methods for screening or purifying ligands which specifically bind to the polypeptides are also provided. The polynucleotides are useful for treating diseases associated with the altered expression of a gene that is coexpressed with one or more known atherosclerosis-associated genes in a subject. They are
 72 GlyHisThrAlaIleLeuAlaProAsnArgTrp......GlnGl
 Composition comprising atherosclerosis-associated polynucleotide useful in diagnosis, prognosis, treatment, and prevention of atherosclerosis and stroke, myocardial infarction, or hypertension
 55 rgPheGlySerAlaAspSerIleSerPheMetIleValValIleLysPhe
 22 CysValSerThrGlyAsnValAlaMetLysGluGlnAsnGlnGlnThrI1 38
 (INCY-) INCYTE GENOMICS INC.
 uIleLeuSerLeuIleIleSerPhe...LeuTrpValLys
 GCTGCGTTCCACTGTGTCAGGATTCTGCATGTGGGTGGAG
 TGAAAAACTCAGTTTCTCCTGTTTACTAAATATTTATTTCATCAACATGG
 GATGGTTCAACTAAGACATGATCACTAAAAACATTATAATAATACCTTTT
 eGluGlnThrIleIleLysGlyLysThrAsnLysGlnGluIleSerSerA
 1; Page 39; 58pp; English
 Volkmuth W,
 (first entry)
 AAC85071
 99US-0349015
 69.50
1.418
61.250
 Walker MG
 from: 1
 Gaps:
Percent Identity:
 ВP
 ţo:
 Length:
 80
2
25.000
 96
 39
 84
 55
 345
 71
 295
 245
```

: .

| \$\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | XXX XX X X X X X X X X X X X X X X X X                                                         |
|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|------------------------------------------------------------------------------------------------|
| 25-FEB-1999<br>09-MAR-1999<br>23-MAR-1999<br>23-MAR-1999<br>01-APR-1999<br>01-APR-1999<br>01-APR-1999<br>11-APR-1999<br>11-APR-1999<br>11-APR-1999<br>21-APR-1999<br>23-APR-1999<br>23-APR-1999<br>30-APR-1999<br>30-APR-1999<br>30-APR-1999<br>30-APR-1999<br>30-APR-1999<br>30-APR-1999<br>30-APR-1999<br>30-APR-1999<br>30-APR-1999<br>30-APR-1999<br>30-APR-1999<br>30-APR-1999<br>30-APR-1999<br>30-APR-1999<br>30-APR-1999<br>30-APR-1999<br>30-APR-1999<br>30-APR-1999<br>30-APR-1999<br>30-APR-1999<br>30-APR-1999<br>30-JUN-1999<br>30-JUN-1999<br>30-JUN-1999<br>30-JUN-1999<br>30-JUN-1999<br>30-JUN-1999<br>30-JUN-1999<br>30-JUN-1999<br>30-JUN-1999<br>30-JUN-1999<br>30-JUN-1999<br>30-JUN-1999<br>30-JUN-1999<br>30-JUN-1999<br>30-JUN-1999<br>30-JUN-1999<br>30-JUN-1999<br>30-JUN-1999<br>30-JUN-1999<br>30-JUN-1999<br>30-JUN-1999<br>30-JUN-1999<br>30-JUN-1999<br>30-JUN-1999<br>30-JUN-1999<br>30-JUN-1999<br>30-JUN-1999<br>30-JUN-1999<br>30-JUN-1999<br>30-JUN-1999<br>30-JUN-1999<br>30-JUN-1999<br>30-JUN-1999<br>30-JUN-1999<br>30-JUN-1999<br>30-JUN-1999<br>30-JUN-1999<br>30-JUN-1999<br>30-JUN-1999<br>30-JUN-1999<br>30-JUN-1999<br>30-JUN-1999<br>30-JUN-1999<br>30-JUN-1999<br>30-JUN-1999<br>30-JUN-1999<br>30-JUN-1999<br>30-JUN-1999<br>30-JUN-1999<br>30-JUN-1999<br>30-JUN-1999<br>30-JUN-1999<br>30-JUN-1999<br>30-JUN-1999<br>30-JUN-1999<br>30-JUN-1999<br>30-JUN-1999<br>30-JUN-1999<br>30-JUN-1999<br>30-JUN-1999<br>30-JUN-1999<br>30-JUN-1999<br>30-JUN-1999<br>30-JUN-1999<br>30-JUN-1999<br>30-JUN-1999<br>30-JUN-1999<br>30-JUN-1999<br>30-JUN-1999<br>30-JUN-1999<br>30-JUN-1999<br>30-JUN-1999<br>30-JUN-1999<br>30-JUN-1999<br>30-JUN-1999<br>30-JUN-1999<br>30-JUN-1999<br>30-JUN-1999<br>30-JUN-1999<br>30-JUN-1999<br>30-JUN-1999<br>30-JUN-1999<br>30-JUN-1999<br>30-JUN-1999<br>30-JUN-1999<br>30-JUN-1999<br>30-JUN-1999<br>30-JUN-1999<br>30-JUN-1999<br>30-JUN-1999<br>30-JUN-1999<br>30-JUN-1999<br>30-JUN-1999<br>30-JUN-1999<br>30-JUN-1999<br>30-JUN-1999<br>30-JUN-1999<br>30-JUN-1999<br>30-JUN-1999<br>30-JUN-1999<br>30-JUN-1999<br>30-JUN-1999<br>30-JUN-1999<br>30-JUN-1999<br>30-JUN-1999<br>30-JUN-1999<br>30-JUN-1999<br>30-JUN-1999<br>30-JUN-1999<br>30-JUN-1999<br>30-JUN-1999<br>30-JUN-1999<br>30-JUN-1999<br>30-JUN-1999<br>30-JUN-1999<br>30-JUN-1999<br>30-JUN-1999<br>30-JUN-1999<br>30-JUN-1999<br>30-JUN-1999<br>30-JUN-1999<br>30-JUN-1999<br>30-JUN-1999<br>30-JU | protein identimetabolic path Arabidopsis the EP1033405-A2. 06-SEP-2000. 25-FEB-2000; 2         |
| 99US-0121825 99US-0125788 99US-0125788 99US-0126564 99US-0126785 99US-0128714 99US-013047 99US-013044 99US-013041 99US-013144 99US-013248 99US-0132486 99US-0132486 99US-0132486 99US-0132486 99US-0132486 99US-0132486 99US-0132487 99US-0132487 99US-0132487 99US-0134219 99US-0134219 99US-0134219 99US-0134214 99US-0134214 99US-0134214 99US-0134214 99US-0134214 99US-013424 99US-013425 99US-013425 99US-013425 99US-013426 99US-013425 99US-013426 99US-013425 99US-013425 99US-013425 99US-013425 99US-013425 99US-013425 99US-013425 99US-013425 99US-013425 99US-013945                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | tification; signal transduction pathway; ithway; promoter; termination sequence; ss. thallana. |
| אין                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | ק<br>גק<br>גק<br>גק<br>גק<br>גק<br>גק<br>גק                                                    |
| 13-JUL-1999; 16-JUL-1999; 16-JUL-1999; 16-JUL-1999; 19-JUL-1999; 19-JUL-1999; 19-JUL-1999; 19-JUL-1999; 19-JUL-1999; 19-JUL-1999; 20-JUL-1999; 21-JUL-1999; 22-JUL-1999; 22-JUL-1999; 22-JUL-1999; 22-JUL-1999; 22-JUL-1999; 22-JUL-1999; 23-JUL-1999; 23-JU                                                                                                                                                                                                                                                                                                                           |                                                                                                |
| 990S-0143542. 990S-0144085. 990S-0144085. 990S-0144085. 990S-0144085. 990S-0144331. 990S-0144333. 990S-0144333. 990S-0145086. 990S-0145086. 990S-0145087. 990S-0145218. 990S-0147204. 990S-0149368. 990S-0149368. 990S-0149368. 990S-0151066. 990S-0151066. 990S-0151086. 990S-0151080. 990S-0151080. 990S-0151080. 990S-0151080.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | -014069<br>-014128<br>-014218<br>-014218<br>-014239<br>-014239                                 |

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US-10-048-197-2 x AAC43179
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 Quality:
Ratio:
Percent Similarity:
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13-SEP-1999
13-SEP-1999
14-SEP-1999
20-SEP-1999
23-SEP-1999
24-SEP-1999
24-SEP-1999
24-SEP-1999
05-OCT-1999
06-OCT-1999
07-OCT-1999
11-OCT-1999
 331
 281
 231 CACCGTCCTCGTTACCGGTGCCGGTGGAAGAACAGGACAAATTGTGTATA
 181
61 rIleSerPheMetIleValValIleLysPheGlyHisThrAlaIleLeuA 78
 45
 30
 3 AsnHisHisIleArgLeuThrIleSerAlaLeuLeuThr......
 GlyLysThrAsnLysGlnGluIleSerSerArgPheGlySerAlaAspSe 61
 .AlaLeuLeuValThrGlyCysValSer...ThrGlyAsnValAla....
 \dots ... \texttt{MetLysGluGlnAsnGlnGlnThrIleGluGlnThrIleIleLys}
 AACAGAAGAGTATCGGTTACCGTTTCCGCCGCCAACAACTGAACCTCT
 ç
O:
 99US-0159331

99US-0159638

99US-0159584

99US-0160761

99US-0160767

99US-0160814

99US-0160814

99US-0160814

99US-0160814

99US-0160980

99US-0160981

99US-0161404

99US-0161405

99US-0161405

99US-0161405

99US-0161405

99US-0161405

99US-0161405

99US-0161405

99US-0161359

99US-0161361

99US-0161361

99US-0161361

99US-0161361

99US-0161361

99US-0161361

99US-0161361

99US-0161361
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990S-0155193
990S-0155486
990S-0155459
990S-0156458
990S-0156596
990S-0157753
990S-0157753
990S-0158029
990S-0158029
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99US-0159295
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0.952
47.097
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 3-0154018.
3-0154039.
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 Percent Identity:
 to: 1014
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 155
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: 23.226
 44
 280
 230
 29
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seq_name:
 07-JUN-1995;
21-APR-1995;
07-JUN-1995;
 Haemophilus influenzae Rd genome medium - useful for identifying fragments by homology searching
 Claim 1; Page 77.2-77.1091; 1291pp; English.
 WPI; 1996-485782/48.
 24-OCT-1996.
 Adams MD,
 (HUMA-) HUMAN GENOME SCI INC (UYJO) UNIV JOHNS HOPKINS.
 22-APR-1996;
 W09633276-A1
 Haemophilus influenzae.
 organism; open
 expression modulating fragment;
 Genome; bacterium; Haemophilus influenzae;
 Haemophilus influenzae complete genome sequence
 554 AGAAGAATCAGATAGACGCTGGTGTTGATGATGATGGATTGTCGTTTGTT
 14-SEP-1999
 AAT42063;
 604
 107
 101
 504
 100
 454
 407
 369
 95
 78
 GTAACAGCTAAGGCT 618
 ValLysProTyrArgPro.....
 LeuThrAlaLysAla
 GTTCTTCTTTGATGATGGAGCTTATCCAGAACAGGTTGACTGGATTGGTC
 CTCCT...GCTGTTGAAGGGATTGATGCTTTGGTCATTCTTACTAGCGCT 453
 laProAsnArgTrpGlnGluIleLeuSerLeuIleIleSerPheLeuTrp
 ..LysAsn......
 GTTCCGCAGATGAAGCCCGGTTTTGATCCTAGTAAAGGAGGAAGACCTGA 503
 Α.....
 /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT:AAT42063
 Fleischmann RD,
 (first entry)
 95US-0487429.
95US-0426787.
95US-0476102.
 reading
 96WO-US05320
 111
 frame; ORF; ds.
 Smith HO,
 regulation; gene expression;
 recorded on commercially
 LeuSerPheTyr 106
 Venter
 computer readable
 computer readable
 important nucleic acid
 JC,
 White
 100
 553
 100
 94
 406
 0
 medium;
vector;
```

This sequence represents the complete genome sequence of the bacterium Haemophilus influenzae strain Rd. The invention relates to a computer readable medium (CRM) having recorded upon it the complete H.influenzae nucleotide sequence (I), a representative fragment of (I) or a nucleotide sequence at least 99% identical to (I). By providing the full-length genomic sequence in a computer readable form, it is possible to identify commercially important nucleic acid fragments and expression modulating fragments (EMFs) of the Haemophilus genome. The EMFs can be used to regulate the expression of a nucleic acid molecule. Vectors and altered organisms comprising the predicted ORFS can be used to produce any of the

predicted ORFS can be used to produce any of the

SXS

Sequence 1830121 BP; 567399 A; 350615 C; 347389 G; 564036 T; 682 other;

polypeptide fragments of the H. influenzae Rd genome

```
alignment_scores:
Quality:
 seq_documentation_block:
ID AAD12599 standard; cDNA; 1155 BP
 alignment_block:
US-10-048-197-2 x AAT42063
 seq_name:
 Align seg 1/1 to: AAT42063
 Percent Similarity:
 260128
 260028
 259978
 259928 TTATCTCGCCATTTTATAGTCTATTTATTTAGCTTATGTGCGATCTTACT
 260078
06-JAN-2000;
06-JAN-2000;
11-JAN-2000;
03-FEB-2000;
03-MAR-2000;
 Homo sapiens.
 haematopolesis; tissue growth activity; Parkinson's disease; cytostatic; Huntington's disease; Alzheimer's disease; Chemotactic; Chemokinetic; haemostatic; thrombolytic; tumour growth inhibitor; anabolic; contraceptive; antiinfertility; antiinflammatory; ss.
 cell proliferation; immunomodulatory; autoimmune disorder; antimicrob multiple sclerosis; rheumatoid arthritis; insulin-dependent diabetes;
 28-DEC-2000;
 12-JUL-2001.
 WO200149728-A2
 Human; hydrophobic domain; gene therapy; nutritional supplement;
 Human protein having hydrophobic domain encoding cDNA clone HP10790.
 25-SEP-2001
 28
 18 uValThrGlyCys......ValSerThrGlyAsnV
 51
 ₩
 2 LeuAsnHisHisIleArgLeuThrIleSerAlaLeuLeuThrAlaLeuLe
 TCGTGTTGGCTGAACAAAACCCCGAATACTCACTTTGAACAAGAAGTGATG
 alAlaMetLysGluGlnAsnGlnGlnThr........
 ACGCGCATCG 260137
 ATCGTGCGATTAAGCCAAGTACTACTGGTTGGAAAAATGAGTAATGAAGA 260127
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 CCTTGCTGGCTGTTCAGTCTAGGGGCGGTTTTGTGTCTAAAAATCATG
 ulleSerSer 54
 /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:AAD12599
 Ratio:
2000JP-0000585.
2000JP-0000588.
2000JP-0002299.
2000JP-0026862.
2000JP-0058367.
 2000WO-JP09359
 (first entry)
 /*tag= a
/product= "Human protein having hydrophobic domain"
/note= "CDS is specifically is claimed in claim 3"
 Location/Qualifiers
 69.50
1.655
60.000
 from: 1
 Percent
 .
6
 Identity:
 Length:
Gaps:
 autoimmune disorder; antimicrobial;
 1830121
 27.143
 20
 28
 51
 37
 260077
 259977
 18
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alignment_block:
US-10-048-197-2 x AAD12599/rev
 alignment_scores:
 polynucleotides and its complementary sequences may also be used as DNA comprehensial production of antibodies in diagnostic assays and also used in gene therapy. The polypeptides may also be used as antigens in the production of antibodies and in assays to identify modulators of polypeptide expression and activity. The polypeptides and nucleic acids may be used as nutritional supplements, to modulate cytokine and cell proliferation activity to modulate immune stimulation or suppression (e.g. for the treatment of microbial infections and autoimmune disorders such as multiple sclerosis, rheumatodid arthritis and insulin dependent diabetes), to modulate tissue growth activity (e.g. for the the composition of Parkinson's disease, Huntington's disease and Alzheimer's disease), to modulate activin and inhibit activity (e.g. for controlling fertility), to modulate chemotactic and chemokinetic activity, to modulate receptor ligand activity, to modulate inflammation and to inhibit tumour growth.
Align seg 1/1
 Percent Similarity:
 (PROT-)
(SAGA)
 The present sequence is human protein with hydrophobic domain encoding cDNA clone HP10790. The polynucleotide and polypeptide of the invention may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate polypeptide expression. The polynucleotides may be used to produce the polypeptide, by inserting the nucleic acids into a host cell and culturing the cell to express the protein. The
 Human proteins with hydrophobic domains and the nucleic acids encoding them, useful for preventing diagnosing and treating e.g. cancer,
 Sequence 1155 BP;
 Claim 4; Page 469-471; 563pp; English
 Alzheimer's and inflammation
 Kato S,
 2001-418355/44
 Quality:
 PROTEGENE INC
SAGAMI CHEM R
 Ratio:
to reverse of: AAD12599
 69.00
1.643
57.534
 280 A;
 RES
 265 C; 274 G; 336 T; 0 other;
 Percent
 Gaps:
Identity:
from: 1
 73
4
32.877
to: 1155
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797
 841
 891 CATGTCCAGGTCACAGTATCCAGCTTGTTTGGGTATCTGAGGAGGACTGG
 756
 51
 38
 5
 21 yCysValSerThrGlyAsnValAlaMetLysGluGlnAsnGlnGlnThrI
 5 HisIleArgLeuThrIleSerAlaLeuLeuThrAlaLeuLeuValThrGl
TATTTCATTTATTGTGTTT
 tIleValValIleLysPhe
 GluIleSerSerArgPheGlySerAla.....AspSerIleSerPheMe 65
 leGluGln......ThrIleIleLysGlyLysThrAsnLysGln
 CTGC....ACTGGAACTCCTGGAATGAAGGCTCCTGGTTTAAAAGTAA
 AGTATCTGGGGCCATTCTCCTCCTGATGTTGTTCGCTTTAT
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697
 50
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 842
 21
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seq\_name: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:AAA81456

Align seg 1/1

to reverse of: AAA81456

from: 1 to: 46593

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lnThrIleIleLysGlyLysThrAsnLysGlnGluIleSerSerArgPhe

56

23 lSerThrGlyAsnValAlaMetLysGluGlnAsnGlnGlnThrIleGluG

23 46078 40

40

46127 CGCATCATCGTTTCGGCTGCGTTCGTTGGCGTTGGCATTAGCAGGTTGCGG

7 ArgLeuThrIleSerAlaLeuLeuThrAlaLeuLeuValThrGlyCysVa

```
alignment_scores
 The present invention describes methods of obtaining immunogenic CC proteins from Nelsseria genomic sequences. AAA81453 to AAA82414 CC represent specifically claimed Nelsseria meningitidis genomic DNA sequences; AAA81260 to AAA81303 and AAB35603 to AAB25663 represent CC AAA81259 and AAA81304 to AAA81303 and AAB35603 to AAB25663 represent CC AAA81259 and AAA81304 to AAA81321 represent PCR primers used in the CC AAA81259 and AAA81321 represent PCR primers and AAA81324 to CC AAA81259 and AAA81321 represent PCR primers and AAA81322 represent Nelsseria meningitidis DNA sequences; and AAA81324 to CC AAA81259 and AAA81322 represent Nelsseria meningitidis MenB polynucleotide ORF CC sequences, which are all used in the exemplification of the present CC invention. The nucleic acid sequences, protein sequences, and antibodies composition can be used as a medicant (or in the manufacture of a composition can be used as a medicant (or in the manufacture of a composition of the used as a medicant (or in the manufacture of a composition of a composition due to CC Neisserial bacteria. For example, some of the identified proteins could be components of vaccines against Meningococcus B; against all serotypes; CC and/or against all pathogenic Nelssariae. Identification of sequences CC and/or against all pathogenic Nelssariae. Identification of sequences CC Multivalent vaccines have failed mainly due to antigen tolerance. CC which are not antigenically variable provision of further, complete exposed proteins that may be presumed targets for the immune system and CC which are not antigenically variable or at least more conserved than cother more variable recions.
Ratio:
Percent Similarity:
 Frazer CM, H
Masignani V,
 Sequence 46593
 other more variable regions.
 Isolated nucleotide sequences of Neisseria meningitidis which can be used in the diagnosis and treatment of N. meningitidis infection and other Neisserial infections, for example, N.gonorrhoea -
 Claim 7; Page 260-274; 1760pp; English.
 WPI; 2000-318079/27.
 Rappuoli R, Pizza M;
 09-OCT-1998;
30-APR-1999;
 08-OCT-1999;
 (CHIR) CHIRON CORP.
 Neisseria meningitidis.
 Meningococcus B; MenB; ds.
 Neisseria meningitidis; Neisseria gonorrheae; genome; antigen; vaccine; diagnosis; infection; antibacterial;
 N. meningitidis partial DNA sequence gnm_4 SEQ ID NO:4.
 04-DEC-2000 (first entry)
 AAA81456 standard;
 Quality:
 Hickey E,
Galeotti
 BP;
 98US-0103794
99US-0132068
 99WO-US23573
69.00
1.278
60.674
 11355 A; 13195
 DNA; 46593
 Peterson
C, Mora
Percent Identity:
 , λ
 C; 11355
 Tettelin H, Venter
Ratti G, Scarselli
 G; 10687
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 189
 T; 1 other
 M,
 Scarlato
 <
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alignment\_block: US-10-048-197-2 x AAA81456/rev

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 46027 CGTTTGCCTTGGGCGTCAGCCCAAATGCCGTAAAAATCAGCAACCGCAAC
 30-APR-1999;
08-OCT-1999;
28-FEB-2000;
The present invention describes the full length genome of Neisseria meningitidis B (NMB). The sequences in AAF21544 and AAF21607 to AAF2161 represent fragments of the NMB genomic sequence, as the sequence was too long to go in a record on its own it was split into 8 sequences which overlap each other at the beginning and end of each
 Claim
 Neisseria meningitidis B full length frames are used to detect, treat and
 Pizza M, Hi
Galeotti C,
 WPI; 2000-647603/62.
 08-MAR-2000; 2000WO-US05928
 09-NOV-2000
 Neisseria meningitidis; Neisseria gonorrheae; diagnosis; antigen; detection; infection; gen
 (CHIR) CHIRON CORP.
(GENO-) INST GENOMIC RES.
 Neisseria meningitidis.
 Neisseria meningitidis B nucleotide sequence SEQ ID NO:113
 13-MAR-2001
 AAF21612 standard; DNA; 349980
 90
 73
 57 GlySerAlaAspSerIleSerPheMetIleValVal.IleLysPheGlyH
 ATGCAATTTGTTTGG
 AATGAAGGCATACGCATCAACTTTACCGCAACTGTGGGTAAGCGCGTGAG
 IleSerPheLeuTrp
 isThrAlaIleLeuAlaProAsnArgTrpGlnGluIleLeuSerLeuIle
 7;
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 Appendix A;
 Hickey E,
 2000GB-0004695
 (first entry)
 99US-0132068
99WO-US23573
 Ģ,
 692pp; English.
 Peterson J,
Ratti G, (
 45863
 , Tettelin H,
Scarselli M,
 genome sequence and open reading prevent Neisserial infections -
 eae; immunogenic; vaccine;
gene therapy; antibacteri
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Scarlato V,
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 45978
 antibacterial;
 Masignani V;
Rappuoli R;
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 alignment_block:
US-10-048-197-2 x AAF21612/rev
 alignment_scores:
 seq_name: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:AAA81489
 CC sequence by 49980 bp (i.e. the last 49980 bp of AAF21544 is repeated at CC the beginning of AAF21607, the last 49980 bp of AAF21607 are repeated at CC the beginning of AAF21608, and so on). AAF21545 to AAF21588 encode the CC Neisseria proteins given in AAB58550 to AAB58593, and AAF21589 to CC AAF21606 represent PCR primers which are used in the exemplification of CC the present invention. The NMB genome and fragments from it have CC antibacterial activity, and can be used in vaccines and gene therapy. CC Neisseria nucleic acids, proteins and/or antibodies which binds to the CC proteins can be used in compositions for treating or preventing infection CC due to Neisserial bacteria or as a diagnostic reagent for detecting the presence of Neisserial bacteria or of antibodies raised to Neisserial ECC computers, computer memory, computer storage medium or computer databases can be used in a search to identify open reading frames (ORFs) CC coroding sequences within the NMB genome. The DNA sequences provide CC further opportunities to find antigenic or immunogenic proteins which are used
 Align seg 1/1 to reverse of: AAF21612
 Percent Similarity:
 239147 CGTTTGCCTTGGGCGTCAGCCCAAATGCCGTAAAAATCAGCAACCGCAAC 239098
 239247 CGCATCATCGTTTCGGCTGCGTTCGTTGGCGTTGGCATTAGCAGGTTGCGG 239198
 239047
 Neisseria meningitidis; Neisseria gonorrheae; antigen; vaccine; diagnosis; infection; antiba
 N. meningitidis partial DNA sequence gnm_37 SEQ ID
 04-DEC-2000 (first entry)
 Sequence 349980 BP; 86473 A; 95646 C; 85908 G; 81953 T; 0 other.
 Meningococcus B; MenB;
 AAA81489;
Neisseria meningitidis
 73
 57 GlySerAlaAspSerIleSerPheMetIleValVal.IleLysPheGlyH
 6
 90
 23 lSerThrGlyAsnValAlaMetLysGluGlnAsnGlnGlnThrIleGluG
 AATGAAGGCATACGCATCAACTTTACCGCAACTGTGGGTAAGCGCGTGAG
 CTCAATCAATAATGTAACCGTTTCCGACTAGAAACTTCAGGAACGTGCCG
 CCAATGCTATGTTACCAGTGTAATCAGCACAATCGGCGTTACCACTTCCG 238998
 isThrAlaIleLeuAlaProAsnArgTrpGlnGluIleLeuSerLeuIle 89
 lnThrIleIleLysGlyLysThrAsnLysGlnGluIleSerSerArgPhe 56
 ArgLeuThrIleSerAlaLeuLeuThrAlaLeuLeuValThrGlyCysVa
 ATGCAATTTGTTTGG
 IleSerPheLeuTrp
 Quality:
 Ratio:
 69.00
1.278
60.674
 94
 238983
 ds.
 Length: 89
Gaps: 1
Percent Identity: 28.090
 from: 1
 antibacterial;
 to: 349980
 genome;
 NO:37.
 immunogenic;
identification;
 73
 40
 239148
 23
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alignment\_block: US-10-048-197-2 x AAA81489/rev

Align seg 1/1 to

reverse of: AAA81489

from: 1

ţo:

23

604018

23

lSerThrGlyAsnValAlaMetLysGluGlnAsnGlnGlnThrIleGluG CGCATCATCGTTTCGGCTGCGTTCGTTGGCATTAGCAGGTTGCGG ArgLeuThrIleSerAlaLeuLeuThrAlaLeuLeuValThrGlyCysVa

6

603919

603918 CGTTTGCCTTGGGCGTCAGCCCCAAATGCCGTAAAAATCAGCAACCGCAAC

603869

lnThrIleIleLysGlyLysThrAsnLysGlnGluIleSerSerArgPhe

6

alignment\_scores:
 Quality:

Sequence 837096 BP; 207534 A; 227065 C;

205215 G; 197280 T; 2 other

Ratio: Percent Similarity:

69.00 1.278 60.674

Length: Gaps: Percent Identity:

: 89 : 1 : 28.090

```
be components of vaccines against Meningococcus B; against all serotypes; and/or against all pathogenic Neissariae. Identification of sequences from the bacterium will also facilitate production of biological probes, particularly organism-specific probes. Attempts to make efficacious Meningococcus B vaccines have failed mainly due to antigen tolerance. Multivalent vaccines have also been tried but none have successfully overcome antigenic variability. The provision of further, complete sequences may provide an opportunity to identify secreted or surface exposed proteins that may be presumed targets for the immune system and which are not antigenically variable or at least more conserved than other more variable.
 AAA81452 represent Neisseria meningitidis MenB polynucleotide ORF sequences, which are all used in the exemplification of the present invention. The nucleic acid sequences, protein sequences, and antibodies against them, can be used in the manufacture of a composition. The composition of a medicament (or in the manufacture of a medicament) for treating, preventing or diagnosing infection due to Neisserial bacteria. For example, some of the identified proteins could
 The present invention describes methods of obtaining immunogenic proteins from Neisseria genomic sequences. AAA81453 to AAA82414 represent specifically claimed Neisseria meningitidis genomic DNA sequences; AAA81260 to AAA81303 and AAB25620 to AAB25663 represent
 Neisseria DNA sequences and their corresponding proteins; AAA81254 to AAA81259 and AAA81304 to AAA81321 represent PCR primers used in the isolation of Neisseria meningitidis DNA sequences; and AAA81322 to
 Isolated nucleotide sequences of Neisseria meningitidis which used in the diagnosis and treatment of N. meningitidis infectiother Neisserial infections, for example, N.gonorrhoea -
 09-OCT-1998;
30-APR-1999;
 Claim 7; Page 629-865; 1760pp; English
 WPI; 2000-318079/27
 Rappuoli R,
 Masignani V,
 Frazer CM,
 08-OCT-1999;
 20-APR-2000
 (CHIR) CHIRON CORP
 Hickey
 Pizza M;
 ickey E,
Galeotti
 98US-0103794
99US-0132068
 99WO-US23573
 Peterson
C, Mora
 ጃ (4
 Tettelin
Ratti G,
 H, Venter
Scarselli
 intection
 Z
 Scarlato V;
 can
 n be
and
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seq_documentation_block:
ID ABA03041 standard; DN
AC ABA03041;
XX
AC ABA03041;
XX
DT 05-FEB-2002 (first e
EX Listeria monocytogene
KW Antibacterial; gene t
KW Antibacterial; gene t
KW Antibacterial gene t
KW Vitamin B12; bacteria
OS Listeria monocytogene
KW Antibacterial gene t
KW Vitamin B12; bacteria
OS Listeria monocytogene
EX NO200177335-A2.

PD 18-OCT-2001; 2001W0-F
XX
I1-APR-2000; 2000FR-0
XX
I1-APR-2000; 2000FR-0
XX
I1-APR-2000; 2000FR-0
XX
Dominguez-Bernal G,
Chakraborty T, Doman
PO LOBERT OF
 seq_name:
 603868
 Chakrau.....J, bay...
Perez-Diaz J, bay...
Maduenio E, De Pablos B
Maduenio E, Voss H;
 The present sequence is the genome sequence of Listeria monocytogenes EGD-e. This sequence and fragments of this sequence are useful for selecting probes and primers for detecting genes in L. monocytogenes and related organisms, and to study genetic polymorphisms and other genomes. Proteins (ABB47297-ABB50149) expressed from the present sequence are useful for raising specific antibodies, identification of L. monocytogenes and related organisms, and for biosynthesis and biodegradation, especially biosynthesis of Vitamin B12. This sequence and proteins encoded by it are also useful for selecting compounds that monocytogenes related diseases. In addition, this sequence and proteins encoded by it are useful in pharmaceutical and vaccines compositions for the treatment or prevention of infections by L. monocytogenes and related
 at ftp.wipo.int/pub/published_pct_sequences
 Note: The sequence data specification, but was o
 Buchrieser C, Frangeul L, Couve E, Rusnick C, Fsihi H, Dehoux P, Dussurget O, Chetouani F, Nedjari H, Glaser P, Kunst F, Cossart Daniels J, Goebel W, Kreft J, Kuhn M, Ng E, Vazquez-Boland JA, Dominguez-Bernal G, Garrido-Garcia P, Tierrez-Martinez A, Amend A, Chakraborty T, Domann E, Hain T, Berche P, Charbit A, Durant L, Perez-Diaz J, Baquero F, Garcia Del Portillo F, Gomez-Lopez N, Maduenio E, De Pablos B, Wehland J, Kaerst U, Entian K, Hauf J;
 Claim 1; SEQ ID No 1; 192pp; French.
 Genomic sequence for Listeria monocytogenes, useful e.g. for and prevention of Listeria and related bacterial infections,
 11-APR-2001; 2001WO-FR01118
 Listeria monocytogenes
 Antibacterial; gene therapy; vaccine; biosynthesis; biodegradation; vitamin B12; bacterial infection; disease; ds.
 (INSP) INST PASTEUR.
 Listeria monocytogenes EGD-e
 ABA03041 standard; DNA; 2944528
 90
 73
 57
 IleSerPheLeuTrp::::::|||
ATGCAATTTGTTTGG
 CCAATGCTATGTTACCAGTGTAATCAGCACAATCGGCGTTACCACTTCCG
 {\tt isThrAlaIleLeuAlaProAsnArgTrpGlnGluIleLeuSerLeuIle}
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 /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:ABA03041
 2000FR-0004629
 (first entry)
 603754
 a for this pa
obtained in
 genome sequence
 patent did not
in electronic fo
 ВP
 ot form part of the printed format directly from WIPO
 603769
 89
 for
 Amend A;
 treatment and
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seq_documentation_block:
 alignment_block:
US-10-048-197-2 x ABA03041/rev
 g
 Align seg 1/1 to
 Percent Similarity:
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 1863652TGGATAAGTGAAATGATTCCTTTCGCATGCGCTAAAATCCCAGTATCAAT
 1863702CACCATGCGCATGCGTTAATAAAATCCGTTTTAACGGTGATTTTAATTTA 1863653
 23-APR-1999;
28-APR-1999;
30-APR-1999;
30-APR-1999;
04-MAY-1999;
05-MAY-1999;
06-MAY-1999;
07-MAY-1999;
 09-MAR-1999
23-MAR-1999
25-MAR-1999
29-MAR-1999
01-APR-1999
06-APR-1999
08-APR-1999
11-APR-1999
21-APR-1999
23-APR-1999
 Hybridisation assay; genetic mapping; gene expression protein identification; signal transduction pathway;
 25-FEB-1999;
05-MAR-1999;
 25-FEB-2000;
 Arabidopsis thaliana.
 metabolic pathway; promoter; termination sequence;
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 17-OCT-2000
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 4 HisHisIleArgLeuThrIleSerAlaLeuLeuThrAlaLeuLeuValTh 20
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 2000EP-0301439
 (first entry)
99US-0128714.
99US-0129845.
99US-0130449.
99US-0130510.
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99US-0131449.
99US-0132484.
99US-0132484.
99US-0132485.
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99US-0132486.
99US-0132486.
99US-0132486.
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99US-0125788.
99US-0126264.
99US-0126785.
99US-0127462.
99US-0128234.
 reverse of: ABA03041
 99us-0121825
 68.50
1.851
75.510
 Percent
 Length:
Gaps:
t Identity:
 from: 1
 49
1
34.694
 ;
O:
 2944528
 1863603
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| 14 - MAX 1999 19 - MAY 1999 20 - MAY 1999 21 - MAY 1999 22 - MAY 1999 22 - MAY 1999 23 - MAY 1999 24 - MAY 1999 26 - MAY 1999 27 - MAY 1999 27 - MAY 1999 28 - JUN 1999 29 - JUN 1999 21 - JUN 1999 22 - JUN 1999 23 - JUN 1999 24 - JUN 1999 25 - JUN 1999 26 - JUN 1999 27 - JUN 1999 28 - JUN 1999 29 - JUN 1999 21 - JUN 1999 21 - JUN 1999 22 - JUN 1999 23 - JUN 1999 24 - JUN 1999 25 - JUN 1999 26 - JUN 1999 27 - JUN 1999 28 - JUN 1999 29 - JUN 1999 20 - JUN 1999 21 - JUN 1999 22 - JUN 1999 23 - JUN 1999 24 - JUN 1999 25 - JUN 1999 26 - JUN 1999 27 - JUN 1999 28 - JUN 1999 29 - JUN 1999 20 - JUN 1999 21 - JUN 1999 22 - JUN 1999 23 - JUN 1999 23 - JUN 1999 24 - JUN 1999 25 - JUN 1999 27 - JUN 1999 27 - JUN 1999 28 - JUN 1999 29 - JUN 1999 20 - JUN 1999 21 - JUN 1999 22 - JUN 1999 23 - JUN 1999 24 - JUN 1999 25 - JUN 1999 27 - JUN 1999 27 - JUN 1999 28 - JUN 1999 28 - JUN 1999 29 - JUN 1999 20 - JUN 1999 21 - JUN 1999 21 - JUN 1999 22 - JUN 1999 23 - JUN 1999 24 - JUN 1999 25 - JUN 1999 26 - JUN 1999 27 - JUN 1999 28 - JUN 1999 28 - JUN 1999 28 - JUN 1999 29 - JUN 1999 20 | -мау-199 |
| 990S-013476. 990S-013476. 990S-013476. 990S-013533. 990S-013533. 990S-013533. 990S-013632. 990S-013632. 990S-013632. 990S-013632. 990S-0137528. 990S-0139456. 990S-0139456. 990S-0139456. 990S-0139456. 990S-0139466. 990S-0139466. 990S-014946. 990S-014946. 990S-014946. 990S-014946. 990S-014946. 990S-014946. 990S-014946. 990S-014946. 990S-014946. 990S-014948. 990S-014948. 990S-01493.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | ži<br>Š  |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |          |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |          |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |          |
| ר די סיסי סיסי סיסי סיסי סיסי סיסי סיסי                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | PR       |
| 27-JUL 1999 28-JUL 1999 28-JUL 1999 28-JUL 1999 28-JUL 1999 29-AUG 1999 20-AUG 1999 20-AUG 1999 20-AUG 1999 20-AUG 1999 20-AUG 1999 20-AUG 1999 21-AUG 1999 22-AUG 1999 23-AUG 1999 24-SEP 1999 25-AUG 1999 26-AUG 1999 27-AUG 1999 28-SEP 1999 29-SEP 1999 21-OCT 1999 22-OCT 1999 23-OCT 1999 23-OCT 1999 24-OCT 1999 25-OCT 1999                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | .199     |
| 990S-0145911 990S-0145911 990S-0145911 990S-0146388 990S-0147308 990S-0147204 990S-0147204 990S-0147493 990S-0147416 990S-0147416 990S-0148319 990S-0148319 990S-0148319 990S-0148319 990S-01483684 990S-0149723 990S-0149723 990S-0149723 990S-0149723 990S-0149723 990S-0149723 990S-0149723 990S-0149723 990S-0151066 990S-0151066 990S-0151066 990S-0152363 990S-0152363 990S-0152363 990S-0152363 990S-0159336 990S-0159336 990S-0159336 990S-0159331 990S-0160761 990S-0160761 990S-0160761 990S-0160981                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | 9us-01,  |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |          |

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US-10-048-197-2 x AAC37886/rev
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 Ratio:
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PR
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PR
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PR
 Align seg 1/1 to reverse of: AAC37886
 Percent Similarity:
New nucleic acid that is a
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P-PSDB; AAB54418.
 Rosen CA,
 12-MAR-1999;
 08-MAR-2000; 2000WO-US05989
 detection; diagnosis; identification; cytostatic; neuroprotective; nootropic; immunomodulatory; relaxant; contraceptive; gynaecological; antiinflammatory; cardiant; gene therapy; chromosome mapping; linkage analysis; tissue identification; tissue typing; forensic; neural; immune system; muscular; reproductive; gastrointestinal; pulmonary; cardiovascular; renal; proliferative; ss.
 25-OCT-1999;
25-OCT-1999;
26-OCT-1999;
26-OCT-1999;
26-OCT-1999;
28-OCT-1999;
28-OCT-1999;
29-OCT-1999;
 (HUMA-) HUMAN GENOME SCI INC
 WO200055320-A1
 Homo sapiens.
 Human pancreatic cancer antigen nucleotide sequence SEQ ID NO:411.
 09-MAR-2001 (first entry)
 Human; pancreas; pancreatic cancer; pancreatic cancer antigen;
 206
 256
 306
 92
 62 eSerPheMetIleValValIleLysPhe......GlyHisThrAlaI 76
 heLeuTrpVaiLysProTyrArgPro 100
 leLeuAlaProAsnArgTrpGlnGluIleLeuSer..LeuIleIleSerP 92
 GTCCTTCATTTTCCTTGCCATCAGGTTCAGGAACTCCGGGAAATCAATGG
 TCTGTTGGGTTTTGCCCCAGAGACCT 181
 TCCCGTTCCCATCTGCATCAACTTCATTGATCATGTCTTGAAGCTCAGCT
 Ruben SM;
 99US-0124270
 99US-0161405.
99US-0161356.
99US-0161356.
99US-0161361.
99US-0161361.
99US-0161920.
99US-0161993.
99US-0161993.
99US-0161993.
 68.00
1.789
64.407
 pancreatic cancer antigen
 Percent
 Identity:
 from: 1
 35.593
 to: 470
 for preventing,
 307
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XX
AC AAC35309;
XX
DT 17-OCT-2000 (first e
XX
DT Arabidopsis thaliana
XX
Hybridisation assay;
 seq_name: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:AAC35309
 alignment_block:
 alignment_scores
 CC neuroprotective, mostropic, immunomodulatory, relaxant, contraceptive, cogynaecological, cardiant and antiinflammatory activities, and can be used CC in gene therapy. The polynucleotide and proteins can be used for CC preventing, treating, or ameliorating a medical condition or in assays Cf or diagnosing a pathological condition or a susceptibility to one in a CC subject. Binding partners to the proteins and the activity of the CC proteins can be identified. The pancreatic cancer antigens can be used to CC detect, treat or prevent pancreatic disorders, especially cancer. CC Agonists and antagonists to the antigens can be screened for. The CC pancreatic cancer antigen polynucleotides can be used to design nucleic caid hybridisation probes that can be used in chromosome mapping, linkage can diagnostic methods. The proteins can be used to generate antibodies can diagnostic methods. The proteins can be used to generate antibodies can diagnostic methods. The proteins can be used to generate antibodies contins can be used to treat or prevent neural, immune system, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal or proteins can be used in the exemplification of the present invention.
 Align seg 1/1 to: AAC99183
 US-10-048-197-2 x AAC99183
 Percent Similarity:
Hybridisation assay; genetic mapping; gene expression control;
 Arabidopsis thaliana DNA fragment SEQ ID NO:
 420
 342
 292 AGTGGGGATGGCTATAATGGATTTGGTAATGATGGAAGCAATTTTGGGAA 341
 242 GTGGTCGTGGTGGCTTTGGTGGCAGCCGTGGTGGTGGTGGATATGGTGGC
 70
 53
 37 ThrileGluGlnThrileIleLysGlyLysThrAsnLysGlnGluIleSe 53
 Sequence 584 BP; 165 A; 99 C; 164 G; 148 T; 8 other;
 AAC98773 to AAC99231 encode the human pancreatic cancer associated proteins, called pancreatic cancer antigens, given in AAB54008 to AAB54466. The human pancreatic cancer antigens have cytostatic,
 Claim 1; Page 845; 1379pp; English.
 24 rThrGly......AsnValAlaMetLysGlu.GlnAsnGlnGln 36
 treating, or ameliorating a medical condition, particular pancreatic cancer, or for use in assays for diagnosing a pathological condition
 8 LeuThrIleSerAlaLeuLeuThrAlaLeuLeuValThrGlyCysValSe
 TTCAAATTTTGGGACCATGAAGGGAAGAAATTTT........
 rSerArgPheGlySerAlaAspSerTleSerPheMetTleValValIleL 70
 GTGGTGGAAGCTACAATGATTTTGGGGGAATTACAACAATCAG.....TC
 GGAAGCAGAACTCTGGCCCTATGGCGGTGGAAGCCAATACTT
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 Quality:
 (first entry)
 68.00
1.333
60.714
 DNA;
 from: 1
 V
 Length: 84
Gaps: 4
Percent Identity: 30.952
 ç
O
 584
 9720.
 385
 291
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|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | protein identification metabolic pathway; pron Arabidopsis thaliana.  EP1033405-A2.  06-SEP-2000.  25-FEB-2000; 2000EP-030  25-FEB-1999; 99US-011  05-MAR-1999; 99US-011  09-MAR-1999; 99US-011  23-MAR-1999; 99US-011  25-MAR-1999; 99US-011  25-MAR-1999; 99US-011  26-APR-1999; 99US-011  16-APR-1999; 99US-011  16-APR-1999; 99US-011  16-APR-1999; 99US-011  21-APR-1999; 99US-011  23-APR-1999; 99US-011  23-APR-1999; 99US-011  23-APR-1999; 99US-011  23-APR-1999; 99US-011  23-APR-1999; 99US-011 |
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| PR 21-JUL-1999 PR 21-JUL-1999 PR 21-JUL-1999 PR 22-JUL-1999 PR 22-JUL-1999 PR 22-JUL-1999 PR 23-JUL-1999 PR 23-JUL-1999 PR 23-JUL-1999 PR 23-JUL-1999 PR 27-JUL-1999 PR 27-JUL-1999 PR 27-JUL-1999 PR 27-JUL-1999 PR 02-AUG-1999 PR 02-AUG-1999 PR 03-AUG-1999 PR 04-AUG-1999 PR 06-AUG-1999 PR 07-AUG-1999 PR 10-AUG-1999 PR 11-AUG-1999 PR 11-AUG-1999 PR 11-AUG-1999 PR 11-AUG-1999 PR 12-AUG-1999 PR 13-AUG-1999 PR 13-AUG-1999 PR 13-AUG-1999 PR 27-AUG-1999 PR 31-AUG-1999 | 24 - JUN - 199 28 - JUN - 199 29 - JUN - 199 30 - JUL - 199 01 - JUL - 199 06 - JUL - 199 08 - JUL - 199 09 - JUL - 199 11 - JUL - 199 12 - JUL - 199 20 - JUL - 199                                                                                       |
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US-10-048-197-2 x AAC35309
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28-OCT-1999
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 30
 07-SEP-1999;
10-SEP-1999;
 3 AsnHisHisIleArgLeuThrIleSerAlaLeuLeuThr.....
 GlyLysThrAsnLysGlnGluIleSer
 AGAAATTGAAGGAGGAGGTCGGAGCAGTTCGTGGCAAGGGGTTTAGTGAGG
 MetLysGluGlnAsnGlnGlnThrIleGluGlnThrIleIleLys 44
 Quality:
 Ratio:
 9903-0160814
9903-0160815
9903-0160981
9903-0160989
9903-0161404
9903-0161406
9903-0161406
9903-0161360
9903-0161361
9903-0161361
9903-0161920
9903-0161920
9903-0161920
9903-0161920
9903-0161920
 990S-0159638
990S-0159638
990S-0160741
990S-0160747
990S-0160768
990S-0160770
 99US-0158232
99US-0158369
99US-0159293
99US-0159294
99US-0159295
99US-0159329
99US-0159330
99US-0159331
 99US-0155659.
99US-0156458.
99US-0156596.
99US-0157117.
99US-0157753.
 99US-0154779.
99US-0155139.
99US-0155486.
 68.00
1.619
71.186
 99us-0158029
 from: 1
 Percent Identity:
 to:
 Length:
Gaps:
 1176
 59
3
28.814
```

seq\_name: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:AAD21310

```
seq_documentation_block:
ID AADZ1310 standard; cDNA; 2144 BP.
XX
AC AADZ1310;
XX
AC AADZ1310;
XX
DT 28-JAN-2002 (first entry)
XX
DE Arabidopsis thaliana SDS cDNA.
XX
KW Meiotic prophase I; chromosome 1; m
KW plant breeding; seed production; SD
OS Arabidopsis thaliana.
XX
FH Key J8..1834
FT CDS 98..1834
FT CDS 98.1834
FT CDS 11-OCT-2001.
XX
FF Key J9.MAR-2000; 20.0005-193523P.
XX
PD 11-OCT-2001.
XX
PF 29-MAR-2000; 2000US-193523P.
XX
PF 29-MAR-2000; 2000US-193523P.
XX
PF 29-MAR-2000; 2000US-193523P.
XX
PR WPI; 2001-662939/76.
PR WAH;
XX
PR WPI; 2001-662939/76.
PR P-PSDB; AAE12998.
XX
PA new plant gene from Arabidopsis, are associated with inability to p production of male sterile plants
CC Alaim 8; Page 39; 47pp; English.
XX
The patent discloses novel plant g designated SDS, which is associate CC conscious attachment during meiotic CC used as a probe to identify relate and to identify some located on chromosome 1 and is used meiosis is bypassed in seed production cc used as a probe to identify relate and cone meiosis is bypassed in seed production of pathway. The present sequence is a SDS protein.
XX
SQ Sequence 2144 BP; 649 A; 461 C; 46
 alignment_block:
US-10-048-197-2 x AAD21310
 alignment_scores:
 Align seg 1/1 to: AAD21310
 Percent Similarity:
 The patent discloses novel plant gene from Arabidopsis thaliana, designated SDS, which is associated with a failure to maintain homologue attachment during meiotic prophase I. The SDS gene is located on chromosome I and is useful in plant breeding to produce male sterile SDS mutants and cloned progeny by apomixis where meiosis is bypassed in seed production. The gene may also be used as a probe to identify related genes in other plant species, and to identify and isolate other genes of the meiosis regulatory pathway. The present sequence is a cDNA encoding Arabidopsis thaliana cne materials.
 A new plant gene from Arabidopsis, designated SDS, mutations in which are associated with inability to produce pollen, is useful for the production of male sterile plants for plant breeding -
 20 hrGlyCysVal.SerThrGlyAsnValAlaMetLysGluGln......
 Meiotic prophase I; chromosome 1; male sterile SD plant breeding; seed production; SDS protein; ss.
CTGGTTGCTTGGGCAGTAAGCAAT.....CAAAAAGAACAAAAAACCCTA 1859
 Quality:
 Ratio:
 68.00
0.958
57.724
 Location/Qualifiers 98..1834
 /*tag= a
/product= "SDS protein"
 chromosome 1; male sterile SDS mutant; apomixis;
 from: 1
 Length: 123
Gaps: 9
Percent Identity: 31.707
 467 G;
 ç
O:
 2144
 567 T; 0 other;
 ω
S
```

3 4

.AsnGlnGlnThrIle.................GluGlnThrIleIleLysG

45

```
seq_documentation_block:
ID AAH17234 standard:
 seq_name: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:AAH17234
 1910
 1860
 29-JUL-1999;
27-AUG-1999;
11-JAN-2000;
02-MAY-2000;
 2110 AAAAAAAAAAAAAAAA
 2010 TGCCACCATTTGTGTCGCTCATACACATTTATTTCTTATTTTCCCTAATT
The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end
 Claim
 Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs -
 07-FEB-2001
 EP1074617-A2
 Human; primer;
 Human
 WPI; 2001-318749/34.
 09-JUN-2000;
 28-JUL-2000; 2000EP-0116126
 Homo sapiens
 26-JUN-2001
 AAH17234;
 (HELI-)
 81
 61
 97
 TTTACAAAACAACACAAGGTAAGTAATAAGAACTCCTCTACAGATTTA 1959
 ProTyrArgProLys 101
 rgTrp...GlnGluIleLeuSerLeuIleIleSerPheLeuTrpValLys
 eValValIleLysPheGlyHisThr....AlaIleLeuAlaProAsnA
 TATACTTAATCGAGCTGGACTTAATTAGCTCTTAGTATACCAATTATTAG
 SerIleSerPheMetIl 66
 AAACCAGGACACAGTATACTCCGATACCAACACACAGGTTATCATTACTA 1909
 lyLysThrAsnLysGlnGluIleSerSerArgPheGlySerAlaAsp...
 Ś
 8; SEQ ID 16615; 2537pp + CD ROM; English
 cDNA sequence
 Isogai T,
, Sugiyama
 HELIX RES INST.
 99JP-0300253.
2000JP-0118776.
2000JP-0183767.
2000JP-0241899.
 (first
 detection; diagnosis; antisense therapy; gene therapy;
 99JP-0248036
 Nishikawa T,
T, Wakamatsu
 CDNA; 2303
 SEQ
 2124
 entry)
 ij
 NO:16615
 ВÞ
 Hayashi K,
A, Nagai K,
 Saito K,
Otsuki
 2109
 96
 2059
 18
 2009
 60
 Yamamoto
 88.
```

(first entry)

Streptococcus 23-OCT-1998

pneumoniae genome

fragment

SEQ

IJ

NO:72

Streptococcus pneumoniae; computer readable medium;

S. pneumoniae; genome; diagnosis; as vaccine; pharmaceutical composition;

seq\_documentation\_block:

AAV52205

standard;

DNA; 14872 BP

seq\_name: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:AAV52205

```
alignment_scores:
Quality:
 CC sequence and an oligonucleotide comprising a sequence complementary to a CC polynucleotide which comprises a 3 -end sequence, where the CC coligonucleotide comprises at least 15 nucleotides and the combination of the 5 -end sequence/3 -end sequence is selected from those defined in CC the primer sets can be used in antisense therapy and in gene therapy. The primer sets can be used in antisense therapy and CC particularly full-length cDNAs. The primers are also useful for the CC detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and CC AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632 crepresent oligonucleotides, all of which are used in the exemplification of the present invention.
 alignment_block:
 US-10-048-197-2 x AAH17234/rev
 Align seg 1/1 to
 Ratio:
Percent Similarity:
 1001
 1101 CTACAATGGGCTGCGGCCTTGGTCGGTCAGCCTTCCTCACTGGGGTAGTC
 1151 CTTAATCATCAGGTGCAGGCTTTCTGCGCTGTCCATACTCTCTACGCTTT
819
 869
 954
 904
 Sequence
 60
 58
 41
 18
 92
 25
 2 LeuAsnHisHisIle.ArgLeuThrIleSerAlaLeuLeuThrAlaLeuL
TTGCTTTGGGTCTAGCCC
 he.LeuTrpValLysPro 97
 GATTTCCCTTTCCCCAATAACTGGCGTAAGATTTTATCAGAATGTTCATCTT
 alleLeuAlaProAsnArgTrpGlnGluIleLeuSerLeuIleIleSerP 92
 AAGGACAGTTTTTCCTGGGTGCAGACA.....TTTTCTGA
 GTGGGATCTTTTAGAATTTCTAGAGGAAGCCTGAGCATCCTGGAATTCC
 erAla....
 CTGCATC...AGCTGTCTCAGCCTGGCTAACTTCAGTTCCCTCTTCTCCA
 rIleIleLysGlyLysThrAsnLysGlnGluIleSerSerArgPheGlyS
 ThrGlyAsnValAlaMetLysGluGlnAsnGlnGlnThrIleGluGlnTh
 euValThrGlyCys.....ValSer
 ...AspSerIleSerPheMetIleValValIleLysPheGlyHisThrAl 75
 2303
 BP;
 reverse of:
 68.00
1.062
51.613
 703 A;
802
 566
 AAH17234
 Gaps:
Percent Identity:
 Ç
 502
 ပ္ပ
 from:
 532
 ۳
 7
 26
 8
 0 other;
 124
6
613
 1052
 1102
 59
 58
 41
 18
```

```
alignment_block:
US-10-048-197-2 x AAV52205
 The present invention describes a computer readable medium which has CC the nucleotide sequences SEQ ID NO:1 to 391 (AAV52134 to AAV52524) CC recorded on it, or a representative fragment or a sequence at least 95% CC identical to SEQ ID NO: 1 to 391. The nucleotide sequences depicted in CC SEQ ID NO:1 to 391 (AAV52134 to AAV52524) are genomic fragments from CC streptococcus pneumoniae. The present invention also describes an CC isolated nucleic acid molecule encoding a homologue of any of the CC isolated nucleic acid molecule encoding a homologue of any of the CC isolated nucleic is produced by a process comprising: (a) screening CC interactive fragments of the Sequences in SEQ ID NO:1 to 391, where the CC isolating the nucleic acid molecules from the members; or (b) isolating the nucleic acid molecules from the members; or (b) isolating CC molecules whose nucleotide sequence is homologous to amplification and isolating the amplified sequences. The computer CC readable medium can be used in a computer-based system for identifying cf fragments of the S. pneumoniae genome. Products pharmaceutical compositions and vaccines for S. pneumoniaes.
 alignment_scores:
 Align seg 1/1 to: AAV52205
 Percent Similarity:
8546 GTTGTGGGGGCGTTGCCCAAGTTGCTATTTCAAAGATTTGTCAAGATAGC
 8496 ACATTTTAGAAGAAGAAGGAAAAAAAATGAGTCGTTTACTAGTTATTG
 8446
 21
 17
 Sequence 14872
 Claim 1; Page 593-602; 1409pp;
 Computer-readable medium with recorded Streptococcus pneumoniae polynucleotide sequences - useful in diagnostic kits and assays, pharmaceutical compositions and vaccines for Streptococcus
 Kunsch
 Barash
 31-OCT-1996;
 30-OCT-1997;
 (HUMA-) HUMAN GENOME SCI INC.
 07-MAY-1998
 Streptococcus
 lyCysValSerThrGlyAsnValAlaMetLysGlu.....GlnAsnGln
 CACTGCAAACTTACACGTGGGAGCCTTTATGTTGCCCCAAGTATGTTGAGG
 HisIleArgLeuThrIleSerAlaLeuLeuThrAla.....
 Quality:
Ratio:
 SC,
 Choi GH,
 BP; 4340 A; 2874 C; 3210 G; 4448 T; 0 other;
 pneumoniae.
 68.00
1.000
56.198
 96US-0029960.
 97WO-US19588
 Dillon
 from: 1
 Percent
 PJ,
 English.
 Length:
Gaps:
Identity:
 to:
 LeuLeuValThrG
 Dougherty BA,
 5
22.314
 Fannon
 8545
 8495
 8595
 35
 21
 16
 and
```

```
seq_name:
 seq_documentation_block:
The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the of an oligonucleotide comprising a sequence comprises a 5'-end sequence and an oligonucleotide comprises a 3'-end sequence complementary to the polynucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises a 3'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in
 29-JUL-1999;
27-AUG-1999;
11-JAN-2000;
 Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs
 Ota T,
Ishii
 8763
 8722
 Claim
 8689
 8596
 WPI; 2001-318749/34.
 8646 TGACTTGAAAGCGAAGCTAGAAGGCAAAACAAGTACTAAAATT.....
 (HELI-)
 09-JUN-2000;
 28-JUL-2000; 2000EP-0116126
 07-FEB-2001.
 EP1074617-A2
 Homo sapiens.
 Human; primer;
 Human cDNA sequence SEQ ID NO:13197.
 26-JUN-2001
 AAH15139;
 AAH15139 standard; cDNA; 1055 BP
 100 oLysAsnLeuSer 104
 84 GluIleLeuSerLeuIleIleSerPheLeuTrpValLysProTyrArgPr 100
 67
 51
 36 GlnThrIleGluGlnThrIleIleLysGlyLysThrAsnLysGln....
 TTTGAATGTAGCT
 GAAGTGATTGCCCTGATTGAAAGCTAC.....AAACCAGAAGCTGT 8762
 alValIleLysPheGlyHisThrAlaIleLeuAlaProAsnArgTrpGln
 GAAACATTTACAGAGATTATGATTGCTAGCCGTACCAAGTCAAAATGCGA 8645
 .GluIleSerSerArgPheGlySerAlaAspSerIleSerPheMetIleV
 8; SEQ ID 13197;
 ß
 /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:AAH15139
 Isogai T,
 HELIX RES INST.
 Sugiyama T,
 ; 99JP-0248036.
; 99JP-0300253.
; 2000JP-0118776.
; 2000JP-0183767.
; 2000JP-0241899.
 (first
 detection; diagnosis; antisense therapy; gene therapy;
 8775
 Nishikawa T,
T, Wakamatsu
 entry)
 GAAACTGCAGCACTTGATGCTGACAAGGTTGAA
 2537pp + CD ROM; English.
 A,
 Hayashi K, :
A, Nagai K,
 Saito K, Y
, Otsuki T;
 Yamamoto
 8721
 83
 8688
 67
 50
 4
 SS
```

```
alignment_scores:
Quali
 888888888888888888
 seq_documentation_block:
ID AAZ51314 standard;
 alignment_block:
US-10-048-197-2 x AAH15139
 seq_name: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2000.DAT:AAZ51314
 Align seg 1/1 to: AAH15139
 Percent Similarity:
 the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH13633 to AAH13742 represent human actid sequences; AAB92446 to AAH3632 represent oligonucleotides, all of which are used in the exemplification
 S. cerevisiae
 871
 821
 771
 721
 697
 657
 607 AACGTGACAGCTGCGTGGAGAAATAATGGTTGGCAACACTTTTCTATTGA 656
 Sequence 1055 BP;
 of the present invention.
 Synthetic
 Saccharomyces cerevisiae
 Yeast delta-9 desaturase; pl-olel gene; oil plant; mono-unsaturated fatty acid;
 06-JUN-2000
 AAZ51314;
 93
 77
 60
 3
 99
 98
 LeuAlaProAsnArgTrpGlnGluIleLeuSerLeuIleIleSerPheLe 93
 spSerIleSerPheMetIleValVallIeLysPheGlyHisThrAlaIle 76
:::|||||||||||:::
 GAAGGGATTTAATTCCAAGCAGAATATTAGCATCCGTTTT.....
 GGATGCATTCCTTTAAATACAGTGCATTACTAAAGTCAGACCTTTTTGAA 820
 eLysGlyLysThrAsnLysGlnGluIleSerSerArgPheGlySerAlaA 60
 AsnValAlaMetLysGluGlnAsnGlnGlnThrIleGluGlnThrIleIl
 GAAAGGCCAAACATTTCCTCCTCCCTTACT 903
 ...ArgProLysAsnLeuSerPheTyrLeuThr 108
 ATAACTTTTTAAAGTCTGTACCGAGTCCTGTTTAACGTAAAATAGCTAGA 870
 u.....TrpValLysProTyr....
 TTATCTTCGGAGGGTTGGAAAGAGTTAAGTGAGTTAGGACTTAGTCATTT 770
 Ratio:
 Lty:
 (first entry)
 delta-9 desaturase gene -
 67.50
1.350
45.045
 Location/Qualifiers
11..1553
/*tag-_a
/transl_except= (pos: 920..922, aa: Leu)
 280 A;
 DNA; 1555
 .CTTGTÅATTAAGTTCAACTTT....TGT 720
 215
 from:
 Percent
 ü
 ВP
 211 G;
 ç
O
 Identity: 27.027
 Gaps:
 349
 yeast; transgenic plant;
foodstuff; ss.
 p1-ole1.
 T; 0 other;
 111
 696
 43
 98
 98
```

```
alignment_block:
 alignment_scores:
 Align seg 1/1
 Percent Similarity:
 US-10-048-197-2 x AAZ51314
 1155
 1105
 1055 ATCAAGTGGTACCAATACGATCCTACTAAAGTGATCATCTACTTGACTTC 1104
 1005 AGGGATACCATAACTTCCATCATGAGTTCCCTACTGATTATAGAAACGCT 1054
 1205 AAGATTAATTGGGGACCTGTTCTTACTGATCTTCCTATGTGGGATAAGCA 1254
 The present sequence is modified yeast delta-9 desaturase pl-olel gene comprising a desaturase domain and a cyt b5 domain, and customised for expression in a plant cytoplasm. This gene is modified for expression in harabidopsis and related species to obtain transgenic plants that produce a higher yield of unsaturated fatty acids. Transgenic plants, especially oil plants, are produced by this method which have increased amounts of unsaturated, particularly mono-unsaturated fatty acids, to obtain foodstuff that is more healthy and has improved flavour.
 New synthetic desaturase gene, useful produce a higher yield of unsaturated expression in a plant cytoplasm -
 Sequence 1555
 Claim 6; Page 71; 77pp; English.
 P-PSDB;
 Martin CE, Mitchell
 24-AUG-1998;
 24-AUG-1999;
 02-MAR-2000.
 W0200011012-A1
 (RUTF) UNIV RUTGERS STATE NEW
 56
 40
 73
 28
 23 lSerThrGlyAsn.....
 7 ArgLeuThrIleSerAlaLeuLeuThrAlaLeuLeuValThrGlyCysVa
IleSerPheLeu 93
 GlnThrIleIleLysGlyLysThrAsnLysGlnGluIleSerSerArgPh 56
 TCTCGTGGGACTTGCTTACGATCTCAAGAAGTTCTCTCAAAACGCTATCG
 AGGAGGCTCTTATCCAACAAGAGCAAAAGAAGATCAACAAGAAGAAGCCT 1204
 eGlySerAlaAspSerIleSerPheMetIleValValIleLysPheGlyH 73
 AACTTTCCTTGCTAAGTCTAAGGAGAACAAGGGACTTGTTATCATCTCTG
 isThrAlaIleLeuAlaProAsnArgTrpGlnGluIleLeuSerLeuIle
 2000-237610/20
DB; AAY70269.
 Quality:
Ratio:
 to: AAZ51314
 BP; 424 A; 336 C;
 98US-0097586
 99WO-US19443
 67.50
1.055
61.538
 /product= "delta-9 desaturase"
 ۶
 from:
 Percent Identity:
 ۳
 JERSEY
 333 G;
 ç
O:
 Length:
Gaps:
 1555
 to obtain transgenic fatty acids, is custo
 462 T; 0 other;
 16.346
 genic plants
customized 1
 1154
 1304
 89
 27
 23
```

that

1305 GAATCGTTCATG

1316

```
alignment_block:
 alignment_scores:
 Align seg 1/1 to:
 US-10-048-197-2 x AAT27729
 Percent Similarity:
 seq_name: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1996.DAT:AAT27729
A DNA fragment (727729) of Haemophilus influenzae includes open reading frames coding for opacity associated proteins OapA (895909) and OapB (895910). It was isolated from the spontaneous opacity variant H175 by cloning SaulAi fragments in lambda EMBL, inflecting E, coli, and screening clones for transforming activity of the opaque type. The oap gene can be used for prodn. of recombinant Oap proteins useful as immunogens for vaccines. Viral vectors including the gene may be developed as live viral vaccines. Detection of H. influenzae in a sample can be performed using the
 documentation_block:
AAT27729 standard; DNA; 2100 BP.
 gene as a probe.
 Claim 4; Fig la-c; 48pp; English.
 Sequence 2100 BP;
 vaccines
 New opacity associated protein of Haemophilus influenzae - and related DNA, vectors, transformed hosts and antibodies, useful
 P-PSDB; AAR95910.
 WPI; 1996-239445/24.
P-PSDB; AAR95909;
 Weiser
 31-OCT-1994;
 24-OCT-1995;
 CDS
 CDS
 (CHIL-) CHILDRENS HOSPITAL PHILADELPHIA.
 09-MAY-1996
 Opacity associated protein; diagnosis; immunogen; ds.
 WO9613515-A1
 Haemophilus influenzae strain Rd variant H175
 Opacity
 17-AUG-1996
 AAT27729;
 Quality:
 Ratio:
 and for diagnosis.
 associated protein gene.
 (first entry)
 AAT27729
 94US-0332576
 67.50
2.045
78.571
 95WO-US13672
 735
 /product= OapB
 /product= OapA
1552..2008
 Location/Qualifiers
 *tag=
 *tag=
 Ą
 Ωı
 396
 from:
 Percent
 Ç
 OapA; OapB; vector;
 μ
 412
 Gaps:
Identity:
 ç
t
 G;
 Length:
 2100
 557
 : 42
: 1
: 33.333
 T; 0 other;
 vaccine;
 antibody;
 in
```

```
CC associated proteins represented in AAB58106 - AAB58548. Lung cancer CC associated proteins represented in AAB58106 - AAB58548. Lung cancer CC associated proteins and polynucleotide sequences, their agonists, and cancer cc antagonists may have neuroprotective; cytostatic; cardioactive; and cimmunomodulatory; muscular active general; vulnerary; gastrointestinal cc general; nephrotropic; antiinfective; gynecological; or antibacterial cc activity. The invention also includes antibodies specific for the creative polynucleotide sequences. The lung cancer associated cc protein or polynucleotide sequences. The lung cancer associated cc polynucleotide sequences may be used for detection of lung cancer, cc diagnostic or research purposes. The proteins may be used to treat cc disorders such as neural, immune, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal, and proliferative cc disorders. The proteins may also be used in the treatment of wounds and confectious diseases. Polynucleotide sequences AAF18425 - AAF18433 and confectious diseases. Polynucleotide sequences AAF18425 - AAF18433 and confection and characterisation of the polynucleotide and protein cc sequences.
 seq_documentation_block:
ID AAF18124 standard;
 seq_name: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2000.DAT:AAF18124
 Claim 1; Page 608-609; 1425pp; English
 1668
 1618
 such as lung cancer
 Lung cancer associated gene sequences, referred antigens, useful for treatment, prevention, and
 P-PSDB;
 Human; lung cancer associated protein; neuroprotective; cytostatic; cardioactive; immunomodulatory; muscular active; vulnerary; gastrointestinal; nephrotropic; antiinfective; gynecological; antibacterial; diagnosis; neural disorder; immune disorder; reproductive; prolliferative disorder; wound healing; infectious disease; ds.
 WPI; 2000-587514/55
 Ruben SM;
 (HUMA-) HUMAN GENOME SCI INC
 12-MAR-1999;
 08-MAR-2000; 2000WO-US05918
 21-SEP-2000.
 WO200055180-A2
 Homo sapiens.
 Lung cancer associated polynucleotide sequence SEQ
 AAF18124 standard; DNA; 3474
 14-MAR-2001
 27
 CCTTACAAAAGGCGAAGCTGATCGA 1693
 TGTAACAACACCTCAAGCGCAAAAAATGCAAGTAGAAAAAGTGGATAAAG 1667
 nValAlaMetLysGluGlnAsnGlnGlnThrIleGlu.......GlnT 41
 AAB58248
 (first entry)
 99US-0124270.
 ВP
 to as lung cancer diagnosis of disorders
 ID 143
```

alignment\_scores:

Sequence 3474

BP; 1062 A;

692 c;

689 G; 1015

T; 16 other

or accelerate wound healing

```
alignment_block:
US-10-048-197-2 x AAF18124/rev
 seq_documentation_block:
 seq_name: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1998.DAT:AAV19980
 Align seg 1/1 to reverse of: AAF18124 from: 1
 Percent Similarity:
 WPI; 1998-159536/14.
P-PSDB; AAW53793.
 Coleman TA, Duan R, J. Ni J, Rampy MA, Ruben
 Keratinocyte growth factor-2; KGF-2; fibroblast growth factor-12; FGF-12; Keratinocyte proliferation; growth stimulator; skin strength; mucositis; epidermal thickening; wound healing; inflammatory bowel disease; therapy; inflammation; hair growth promoter; ds.
 15-JUL-1998 (first entry)
 AAV19980 standard; cDNA; 4177 BP
 471
 509
 Keratinocyte growth factor-2 deletion mutants - useful to promote
 (HUMA-) HUMAN GENOME SCI INC
 28-FEB-1997;
13-AUG-1996;
 13-AUG-1997;
 19-FEB-1998
 WO9806844-A1
 Homo sapiens
 Full length Keratinocyte growth factor-2 coding sequence
 609 TCAGTATCCATTTCCACATTGTACTGAAACTCTCGGCACTGGAAATTGTC 560
 647 GCAGCCGGGCAGGTGG...........GGAAAGGCTGAGGCACAATGTG
 69
 95
 80
 35 nGlnThrIleGluGlnThrIleIleLysGlyLysThrAsnLysGlnGluI 52
 19 ValThrGlyCysValSerThrGlyAsnValAlaMetLysGluGlnAsnGl
 ValLysProTyrArgProLysAsnLeuSerPheTyrLeuThrAlaLys 110
 AGAGCTCGAGGTGG.......CTGCTGGTTAGCTCCCTCTGG 472
 GCGCGGATCTGGCCAGAAGTGAATGCACCAACATCCATAACTCCTCGG
 TCATCAGAAGGAACATACTGGAAGGGTAAGACCCGATGCAAGGCAAGGAG 510
 leSerSerArgPheGlySerAlaAspSerIleSerPheMetIleValVal 68
 AsnArgTrpGlnGluIleLeuSerLeuIleIleSerPheLeuTrp 94
 97US-0039045.
96US-0023852.
 97WO-US14112
 67.50
1.298
52.000
 Location/Qualifiers 593..1219
 Jimenez
en SM, 2
 Percent Identity: 28.000
 Zhang
 ָיס
 Mendrick D,
g J;
 .
6
 648
 610
```

```
alignment_block:
US-10-048-197-2 x AAV19980/rev
 alignment_scores:
 Control of keratinocytes. The mutants of the invention, that stimulate correction is used to create the mutants of the invention, that stimulate corporate is used to create the mutants have enhanced keratinocytes. The mutants have enhanced keratinocytes correctly stimulating activity as compared to wild-type KGF-2 (also known as compared to provide the control of keratinocytes. In particular, they are used to prevent or improve the appearance of wrinkles or aged skin, improving skin control of keratinocytes. In particular, they are used to prevent correctly strength, promoting epidermal thickening, reducing scarring or improving the healing after cosmetic surgery. The mutants are also useful for promoting compared to be treated may be surgical or excisional wounds, deep wounds compared to be treated may be surgical or excisional wounds, deep wounds control of the dermis and epidermis, eye tissue wounds, dental correctly compared through use of the KGF-2 deletion mutants. They can also be achieved through use of the KGF-2 deletion mutants. They can also be achieved through use of the KGF-2 deletion mutants. They can also be calieved treatment or prevention of mucositis, inflammatory bowel contenting tissue exposed to radiation or protecting tissue to be exposed to radiation or protecting tissue to be exposed to radiation (e.g. to allow an increase in radiation dosage used to treat correctly exposed to radiation and increase in radiation dosage used to treat treatment treatment or protecting tissue to be exposed to radiation and increase in radiation dosage used to treatment correctly exposed to treatment or protecting tissue to be exposed to radiation or protecting tissue to be exposed to radiation dosage used to treatment correctly exposed to treatment or protecting tissue to be exposed to radiation dosage used to treatment correctly exposed to treatment or protecting tissue to be exposed to radiation dosage used to treatment correctly exposed to radiation dosage used to treatment correctly exposed to radiation
 seq_name: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1999.DAT:AAZ11169
 Align seg 1/1 to reverse of: AAV19980
 Ratio:
Percent Similarity:
 119
 649 GCAGCCGGGCAGGTGG......GGAAAGGCTGAGGCACAATGTG
 Sequence 4177 BP; 1332 A; 816 C; 874 G; 1155 T; 0 other;
 a malignancy).
 Disclosure; Fig 3; 251pp; English.
 473 GCGCGGATCTGGCCAGAAGTGAATGCACCAACATCCATAACTCCTCGG 426
 511 AGAGCTCGAGGTGGTGG......CTGCTGGTTAGCTCCCTCTGG 474
 561 TCATCAGAAGGAACATACTGGAAGGGTAAGACCCGATGCAAGGCAAGGAG 512
 80
 52 leSerSerArgPheGlySerAlaAspSerIleSerPheMetIleValVal 68
 35 nGlnThrIleGluGlnThrIleIleLysGlyLysThrAsnLysGlnGluI 52
 19 ValThrGlyCysValSerThrGlyAsnValAlaMetLysGluGlnAsnGl
 ValLysProTyrArgProLysAsnLeuSerPheTyrLeuThrAlaLys 110
 AsnArgTrpGlnGluIleLeuSerLeuIleIleSerPheLeuTrp 94
 TCAGTATCCATTTCCACATTGTACTGAAACTCTCGGCACTGGAAATTGTC
 Quality:
 67.50
1.298
52.000
 DNA;
 4177
 Length:
Gaps:
Percent Identity:
 from: 1
 28.000
 to: 4177
 562
 612
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(first entry)

alignment\_block: US-10-048-197-2 x AAZ11169/rev

Align seg 1/1

to reverse of: AAZ11169

from: ب

to: 4177

:

611

52 leSerSerArgPheGlySerAlaAspSerIleSerPheMetIleValVal

TCAGTATCCATTTCCACATTGTACTGAAACTCTCGGCACTGGAAATTGTC

562

79

89

612

512 94

GCAGCCGGGCAGGTGG.......GGAAAGGCTGAGGCACAATGTG nGlnThrIleGluGlnThrIleIleLysGlyLysThrAsnLysGlnGluI

52

650 35

69

649

35

19 ValThrGlyCysValSerThrGlyAsnValAlaMetLysGluGlnAsnGl

alignment\_scores

Quality: Ratio:

67.50 1.298 52.000

Length: Gaps: Percent Identity:

28.000

Percent Similarity:

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CC protein. Fragments and mutants of this sequence are used in the methods CC of the invention, for increasing the level of platelets, fibrinogen, CC albumin, globulin, and total serum protein in the blood. KGF-2 can also be used to stimulate proliferation of salivary gland cells, lacrimal CC gland cells, sinus epithelium, and Goblet cells. The methods can also be used to treat hypofibrinogenaemia caused by a cirrhosis, and disseminated CC intravascular coagulation (DIC). The methods can be used to treat CC caused by: drug induced hypersensitivity, thrombocytopaenia purpura, metastatic tumours in the bone, aplastic CC caused by: drug induced hypersensitivity, thrombocytopaenia purpura, cc megaloblastic anaemia peritonitis, congenital rubella syndrome, cc megaloblastic anaemia peritonitis, congenital rubella syndrome, CC posttransfusion purpura, metastatic tumours in the bone, aplastic CC anaemia, myelofibrosis, leukaemia, haemolytic syndromes, cancer CC megaloblastic anaemia peritonitis, congenital rubella syndrome, CC Epstein Barr infectious mononucleosis, systemic lupus, preeclampsia, CC paterial viral and parasitic infections, tissue necrosis, vasculitis, CC ulcerative bowel disease, serositis, subacute bacterial endocarditis, congestive heart CC syndrome, trauma and crush injuries, gastrointestinal and lymphatic cc syndrome, trauma and crush injuries, gastrointestinal and lymphatic constitue, and protein losing gastroenteropathies. The methods can also be used to treat hypoglobulinaemia, total protein loss, damage to the sinus of the bladder or prostate, stimulate proliferation of the salivary gland cells and to increase Goblet cell proliferation for treating or preventing keratoconjuctivitis sicca.
 disseminated intravascular coagulation; thrombocytopaenia; myelofibrosis; hypoalbuminaemia; posttransfusion purpura; metastatic tumour; anaemia; leukaemia; haemolytic syndrome; Zleve's syndrome; rheumatic disease; HELLP preeclamptic syndrome; congenital rubella syndrome; systemic lupus; Epstein-Barr infectious mononucleosis; thyrotoxicosis; uraemia; therapy; infection; tissue necrosis; vasculitis; ulcerative bowel disease; serositis; subacute bacterial endocarditis; liver disease; amyloidosis; congestive heart failure; constrictive perioarditis; nephrotic syndrome;
 This sequence encodes the human keratinocyte growth factor-2 (KGF-2)
 Disclosure; Fig 3; 331pp; English.
 Use of keratinocyte growth factor-2 to increase levels of platelets, fibrinogen, albumin, globulin and total serum protein
 Jimenez P,
 30-DEC-1998;
13-FEB-1998;
 12-FEB-1999;
 SS.
 (HUMA-)
 19-AUG-1999
 W09941282-A1
 Homo sapiens
 cardiac valvular
 Keratinocyte growth factor; KGF-2; human; platelet; fibrinogen; albumin; globulin; total serum protein; blood; hypofibrinogenaemia; cirrhosis; disseminated intravascular coagulation; thrombocytopaenia; myelofibrosis
 Human keratinocyte growth factor, KGF-2, gene.
 HUMAN GENOME
 Louie A,
 98US-0114387.
98US-0074585.
 99WO-US03018
 failure;
disease;
 Location/Qualifiers 593..1216
 /product= KGF-2
 /*tag=
 SCI INC
 Mendrick D,
 hypoglobulinaemia; keratoconjuctivitis sicca;
 Rampy MA,
 Russell
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426

23

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816 C; 874 G;
 1155 T; 0 other;
 seq_documentation_block:
ID AAA71214 standard; DNA; 4177
XX
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 13-AUG-1996;
28-FEB-1997;
13-AUG-1997;
05-JUN-1995;
 hepatic; respiratory; renal; cerebroprotective; mucositis; treatment; epithelial cell proliferation; inflammatory bowel disease; lung damage; liver disorder; diabetes; oral injury; gastrointestinal injury; gut toxicity; gastric; duodenal; epidermolysis bullosa; skin graft; skin disorder; renal failure; brain injury; intestinal fibrosis; proceptitis, female reproductive tract disorder; pulmonary fibrosis;
 13-FEB-1998;
 US6077692-A
 antiinflammatory; cytoprotective; dermatological; gastrointestinal;
 Homo sapiens.
 pneumonitis; pleural retraction; hemopoletic syndrome; myelotoxicity; ds.
 Human; keratinocyte growth factor; KGF-2; antiulcer; antidiabetic;
 Human
 20-NOV-2000
 AAA71214;
 473 GCGCGGATCTGGCCAGAAGTGAATGCACCAACATCCATAACTCCTCGG
 511 AGAGCTCGAGGTGGTGG......CTGCTGGTTAGCTCCCTCTGG
 561 TCATCAGAAGGAACATACTGGAAGGGTAAGACCCGATGCAAGGCAAGGAG
 95
 80
 ValLysProTyrArgProLysAsnLeuSerPheTyrLeuThrAlaLys 110
 AsnArgTrpGlnGluIleLeuSerLeuIleIleSerPheLeuTrp
 /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:AAA71214
 keratinocyte growth factor KGF-2 genomic DNA SEQ ID NO:
 (first entry)
96US-0023852.
97US-0039045.
97US-0055561.
95US-0461195.
 98US-0023082
 /*tag= a
/product= "KGF-2"
 Location/Qualifiers 593..1219
 ВP
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Sequence 4177 BP; 1332 A;

```
alignment_block:
US-10-048-197-2 x AAA71214/rev
 alignment_scores:
 cc dermatological, gastrointestinal, hepatic, respiratory, renal and cerebroprotective activity. (I) is useful for stimulating epithelial cell cc proliferation in patients suffering from wound, mucositis, ulcer such as cc venous statis ulcer, diabetts ulcer and cubitus ulcer. (I) is also useful cc diabetes, oral injury, gastrointestinal injury, gut toxicity, gastric cc ulcer, duodenal ulcer, epidermolysis bullosa, skin graft, skin disorder, crenal failure, brain injury, breast tissue injury, urothelial damage, cc female reproductive tract disorder, intestinal fibrosis, proctitis, cc pulmonary fibrosis, pneumonitis, pleural retraction, hemopoletic syndrome cc skin grafts to wound beds and to stimulate re-epithelialization from the cwound bed, to produce changes in hepatocyte proliferation, to reduce the cside effects of gut toxicity, to regenerate skin in full and partial continuous enhanced activity, increased stability, higher yield and better cc slubility. This sequence encodes the human KGF-2 protein described in vx
 Percent Similarity:
 Align seg 1/1 to reverse of: AAA71214
 14-FEB-1995;
23-MAY-1997;
13-AUG-1997;
 Novel keratinocyte growth factor useful for promoting and accelerating wound healing, comprising at least 10 contiguous amino acids from a specific amino acid sequence -
 561
 649
 699
 This invention describes a novel human keratinocyte growth factor, KGF-2 (I), which has antiulcer, antidiabetic, antiinflammatory, cytoprotective dermatological, gastrointestinal, hepatic, respiratory, renal and
 Disclosure; Fig 3A-D; 190pp; English.
 511
 611
 Sequence 4177
 P-PSDB; AAB10304.
 Mendrick D,
 (HUMA-) HUMAN
 80
 52 leSerSerArgPheGlySerAlaAspSerIleSerPheMetIleValVal 68
 35
 19
ValLysProTyrArgProLysAsnLeuSerPheTyrLeuThrAlaLys 110
 nGlnThrIleGluGlnThrIleIleLysGlyLysThrAsnLysGlnGluI 52
 AsnArgTrpGlnGluIleLeuSerLeuIleIleSerPheLeuTrp 94
 TCATCAGAAGGAACATACTGGAAGGGTAAGACCCGATGCAAGGCAAGGAG
 TCAGTATCCATTTCGACATTGTACTGAAACTCTCGGCACTGGAAATTGTC
 ValThrGlyCysValSerThrGlyAsnValAlaMetLysGluGlnAsnGl 35
 2000-441307/38:
 Quality:
Ratio:
 Ľď,
 Gentz RL,
 Duan
 BP;
 GENOME SCI INC
 95WO-US01790.
97US-0862432.
97US-0910875.
 67.50
1.298
52.000
 1332 A;
 DR,
 Ni J,
 Ruben SM,
 816 C;
 Percent Identity:
 Jimenez P, (
SM, Zhang J,
 , GGAAAGGCTGAGGCACAATGTG
 874 G; 1155 T; 0 other;
 from: 1 to: 4177
 antiinflammatory, cytoprotective,
 Coleman TA,
Moore PA,
 28.000
 100
 79
 Gruber JR;
Rampy MA;
 512
 612
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Seq_documentation_block:
ID AAF31912 standard; DN
AC AAF31912 standard; DN
AC AAF31912;
XX
DT 10-APR-2001 (first 6
XX Human keratinocyte growth 1
KW mucositis; ulcer; inid
KW Lung damage; diabetes
epidermolysis bullose
pidermolysis bullose
pidermolysis bullose
pidermolysis bullose
kW pulmonary fibrosis; ss.
XX
DI 1-JAN-2001.
XX
PN W0200102433-A1.
XX
PD 11-JAN-2001.
XX
PD 11-JAN-2001.
XX
PD 11-JAN-2001.
XX
PD 11-JAN-2001.
XX
PD 11-JAN-2000; 2000WO-1
PR 12-AUG-1999; 99US-1
PR 13-AUG-1999; 99US-1
PR 13-
 seq_name: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:AAF31912
 The present sequence is a coding sequence for human keratinocyte growth factor (KGF-2). KGF-2 can be used to stimulate epithelial cell proliferation in a patient, where the patient has a wound, mucositis, an ulcer, inflammatory bowel disease, liver disorder, lung damage, diabetes, oral injury, gastrointestinal injury, gut toxicity, epidermolysis bullosa, skin graft, skin disorder, renal failure, brain injury, breast tissue injury, urothelial damage, female reproductive tract disorder, intestinal fibrosis, proctitis, pulmonary fibrosis, peunrumonitis, plural retraction, haemopoietic syndrome, and myelotoxicity. In addition, KGF-2 can be used in the treatment or prevention of ovary injury, infertility, or fibrosis of the liver. KGF-2 also promotes internal healing, donor site healing, internal surgical wound healing or healing of incisional wounds made during cosmetic surgery in a patient.
 Keratinocyte growth factor; KGF-2; epithelial cell proliferation; wound; mucositis; ulcer; inflammatory bowel disease; liver disorder; lung damage; diabetes; oral injury; gastrointestinal injury; epidermolysis bullosa; renal failure; brain injury; proctitis;
 473
 A polynucleotide encoding the human keratinocyte for stimulating epithelial cell proliferation in
 Disclosure; Fig 3; 591pp; English.
 WPI; 2001-071578/08.
P-PSDB; AAB61668.
 pulmonary fibrosis; haemopoietic syndrome;
liver fibrosis; ss.
 (HUMA-) HUMAN GENOME SCI INC
 GCGCGGATCTGGCCAGAAGTGAATGCACCAACATCCATAACTCCTCGG
 99US-0171677.
2000US-0198322.
2000US-0205417.
 2000WO-US18328
 (first entry)
 2000US-9911224
 99US-0143648.
99US-0144024.
99US-0148628.
 99US-0149935
99US-0163375
 99US-0142343
 Coleman
 ۵,
 growth factor coding sequence
 DNA; 4177
 Duan DR, Rampy MA,
nan TA, Gruber JR,
 ВP
 ovary injury; infertility;
 Dillon
 Mendrick D, Zhang J
Dillon PJ, Gentz RL;
 e growth fact
a patients
 426
 factor useful
ents that has
```

alignment\_scores:

Quality:

67.50

100

Sequence 4177 BP; 1332 A; 816 C; 874 G; 1155 T; 0 other;

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ID ABL26466;
XX ABL26466;
XX ABL26466;
XX Drosophila melanogast
XX Drosophila pharmaceutical; gene;
XX PD 27-SEP-2001; 2001WO-I
XX PP 23-MAR-2000; 2000US-I
XX PP 23-MAR-2001; 2001WO-I
XX PP 23-MAR-2000; 2000US-I
XX PP 23-MAR-2000; 2000US
 seq_name: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:ABL26466
 alignment_block:
US-10-048-197-2 x AAF31912/rev
 Align seg 1/1 to reverse of: AAF31912
 Ratio:
Percent Similarity:
The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of
 Claim 1; SEQ ID NO 30871; 21pp + Sequence Listing; English.
 New isolated nucleic acid genes from Drosophila and interactions -
 23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000US-0614150.
 23-MAR-2001; 2001WO-US09231.
 Drosophila melanogaster
 Drosophila; developmental biology; cell signalling; pharmaceutical; gene; ds.
 Drosophila melanogaster genomic polynucleotide SEQ ID NO 30871
 26-MAR-2002 (first entry)
 473
 511
 561
 611
 649
 95
 80
 69
 52 leSerSerArgPheGlySerAlaAspSerIleSerPheMetIleValVal 68
 35 nGlnThrIleGluGlnThrIleIleLysGlyLysThrAsnLysGlnGluI 52
 19
 GCGCGGATCTGGCCAGAAGTGAATGCACCAACATCCATAACTCCTCGG 426
 ValLysProTyrArgProLysAsnLeuSerPheTyrLeuThrAlaLys 110
 AGAGCTCGAGGTGGTGG.........CTGCTGGTTAGCTCCCTCTGG 474
 TCATCAGAAGGAACATACTGGAAGGGTAAGACCCGATGCAAGGCAAGGAG 512
 TCAGTATCCATTTCCACATTGTACTGAAACTCTCGGCACTGGAAATTGTC
 AsnArgTrpGlnGluIleLeuSerLeuIleIleSerPheLeuTrp
 GCAGCCGGCCAGGTGG.......GGAAAGGCTGAGGCACAATGTG
 ValThrGlyCysValSerThrGlyAsnValAlaMetLysGluGlnAsnGl
 1.298
52.000
 DNA; 13239
 Li
 PWD,
 detection reagent for detecting 1000 or more for elucidating cell signalling and cell-cell
 Gaps:
Percent Identity:
 BP.
 Myers
 W
 from: 1
 28.000
 to: 4177
 insecticide
 94
 79
 562
 612
 35
 rs.
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alignment_block:
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 US-10-048-197-2 \times ABL26466/rev
 Align seg 1/1 to reverse of: ABL26466
 Ratio:
Percent Similarity:
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 7775
 7825
 7725 GATTTACCCACCTCCGCAGAGGAATCACCGCCGTAACTGCCATGAATCAT 7676
 7875 CTCGTTATACTGTAGAACAACTATATAGAGAATCGGGCATTGCCCAAGCG
 7925
 7963 ATGCTCGGGGCACATTGTACAATA......CTACACCCAACATT
 insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072).

The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from at ftp.wipo.int/pub/published_pct_sequences.
 82
 67
 54
 45
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 TCCAATTCAAGTTTACGGGTCAGGCAATTCGGTCCAATTCAATCTGCCGT 7726
 ValValIleLysPheGlyHisThrAlaIleLeuAlaProAsnArg 81
 SerArgPheGlySerAlaAspSerIleSerPheMetIle....
 AACCGAACCGGGAGAGATCGGCGAGCGGAGTGGGCGCTTATCAGGAATCA 7776
 snGlnGlnThrIleGluGlnThrIleIleLys.....
 ACATTGCACACATGGGCCAAGTGTGCGTGAGTGTGCGTCGAGATCTCGAT 7876
 GlyLysThrAsnLysGlnGluIleSer......
 Quality:
 1.107
53.509
 Length:
Gaps:
Percent Identity:
 from: 1
 3616
 21.930
 to: 13239
 H,
 0 other;
 66
 7826
 7926
 53
 44
 34
 17
 WIPO
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9b_htg:AC013798
9b_htg:AC0013798
9b_htg:AC002394
9b_htg:AC0023140
9b_htg:AC068980
9b_htg:AC084447
9b_htg:AC0294447
9b_htg:AC039481
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gb_pr:AC097661
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 Results were produced by Copyright (c) 1993-2000
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00 Compugen Ltd.
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AUTHORS
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REFERENCE
AUTHORS
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 * NOTE: This record contains 61 individual

* sequencing reads that have not been assembled into

* contigs. Runs of N are used to separate the reads

* and the order in which they appear is completely

* arbitrary. Low-pass sequence sampling is useful for

* identifying clones that may be gene-rich and allows

* overlap relationships among clones to be deduced.

* However, it should not be assumed that this clone

* will be sequenced to completion. In the event that

* the record is updated, the accession number will

* be preserved.
 Submitted (22-NOV-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
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of 645 bp in length
 bp in length
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Unpublished
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42712 42817
 40494
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 9.00
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others

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HTG 24-NOV-2001 SAMPLING.

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Submitted (24 NOV-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA All repeats were identified using RepeatMasker:
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http://ftp.genome.washington.edu/RM/RepeatMasker.html
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 Contact: sequence_submissions@genome.wi.mit.edu
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of 703 bp in
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 of 684 bp
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of 700 bp in
 of 675 bp in length
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JOURNAL

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1701 bp
100 bp f 687 by 100 bp 188 bp j of 100 bp of 686 100 bp f 706 bp 100 bp f 710 bp 100 bp 100 bp f 695 bp 100 bp 100 bp f 716 bj 100 t 100 bp 100 bp 686 bp in 100 695 100 bp 100 bp 100 bp 100 ) 697 طم د مورد qd • đđ bp in ďď đđ đđ ďq þ φd đđ ďq dq đđ đđ 'n in 'n ij in 'n ä ä in 'n in ij 'n in length in 'n in in 'n in 'n in length in in in in 'n Ħ ij in in in length 
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Waterston, R.H.
 Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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 AC064841 69829 bp DNA linear PRI 01-FEB Homo sapiens chromosome 2 clone CTD-2015A10, complete sequence
 The sequence of Homo sapiens clone Unpublished
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 Direct Submission
Direct Submission
Submitted (31-JAN-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Feb 4, 2002 this sequence version replaced gi:18477451.
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On Feb 1,
Assembly program: XGAP4; Version 4.5
Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 107323 bases at least Q40
Consensus quality: 109309 bases at least Q30
 Center code: WUGSC
 Waterston, R.H.
Direct Submission
Submitted (01-FEB-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St.
 AL670662 113776 bp DNA linear HTG 01-I
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 Center project name: bPG93B10
 Contact: humquery@sanger.ac.uk
Project Information
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 Center project name: H_MS2015A10
 Contact: submissions@watson.wustl.ed
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 3 (bases 1 to 69829)
 Web site: http://www.sanger.ac.uk
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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 Submitted (03-MAR-2000) Genome Analysis, Institute of Molecular Biotechnology, Beutenbergstrasse 11, Jena 07745, Germany
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 Whitehead
 Submitted
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29645
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29745
38379
38479
 soon
 preserved
9ap oc
46868: con
9 46968: gap of
56724: cr
 38378:
3 38478: gan
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 923:
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2980: cc
 92: gap of 100 bp 22474: contig of 6382 bp
 Project Information
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contig of 8634 bp in ap of 100 bp
contig of 8390 bp in ap of 100 bp
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 100 bp
of 7070 bp
 of
 of 823 bp
 MIT Center for Genome Research
 100% of reads
ye; 100% of reads
 gd
 t least Q40
t least Q30
t least Q20
 ď
 agarose-fp
sum-of-contigs
 in length
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68014 68113: gap of 100 bp

68114 80779: contig of 12666 bp ir

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 Submitted (01-FEB-2002) Genome Analysis, Institute of Molecular Biotechnology, Beutenbergstrasse 11, Jena 07745, Germany On Feb 1, 2002 this sequence version replaced gi:7382151. On Jan 22, 2002 this submission replaced accession AC019286 Drafting Center: Whitehead Institute/ MIT Center for Genome
 Wen, G. and Platzer, M. Direct Submission
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 Unpublished
 Homo sapiens
 Quality levels above 40 are expected to have less than 1 error in 10,000 bp.
Base-by-base quality values are not generally visible from GenBank flat file format but are available as part of this entry's ASN.1 file.
 HTG; HTGS_DRAFT; HTGS_ACTIVEFIN.
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All manually edited bases have been reduced to qual
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 Center project name:
 Contact: gscj-submit@genome.imb-jena.de
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 Center: Insitute of Molecular Biotechnology
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10.
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 82041:
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Ratio: 1.000
Percent Similarity: 100.000
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 ATCCTCTCTTAATTATCTCCTTTCTT 109469
 gb_htg:AC106051
168577 bp DNA linear HTG l1-JAN-2002 Homo sapiens chromosome 4 clone RP11-692K15, WORKING DRAFT SEQUENCE, 3 unordered pieces. AC106051 AC055844 AC106051.1 GI:18129600 HTG; HTGS_PHASP1. """"
 Morrow,J., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P., Peterson,K., Pollara,V., Riley,R., Roy,A., Santos,R., Severy,P., Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J., Tesfaye,S., Tirrell,A., Vassiliev,H., Vo,A., Wheeler,J., Wu,X., Wyman,D., Ye,W.J., Zimmer,A. and Zody,M.
 Submitted (23-SEP-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Feb 9, 2002 this sequence version replaced gi:18543112.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
 Wyman, D., Ye, W.J., Direct Submission
 http://ftp.genome.washington.edu/RM/RepeatMasker.html
 48029
 1 12794: contig of 12794 bp in length
12795 12894: gap of 100 bp
12895 68988: contig of 56094 bp in length
68989 69088: gap of 100 bp
69089 133991: contig of 64903 bp in length
133992 134091: gap of 100 bp
134092 162167: contig of 2006 bp in length
162168 162267: gap of 100 bp
162268 165412: contig of 3145 bp in length.
 NOTE: This is a 'working draft' sequence. It currently consists of 5 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
 be preserved.
 Web site: http://www-seq.wi.mit.edu

contact: sequence_submissions@genome.wi.mit.edu

------ Project Information

Center project name: L2720

Center clone name: 3_E_17
 Center: Whitehead Institute/ MIT Center for Genome Research Center code: WIBR
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 Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.990319
Consensus quality: 167893 bases at least Q40
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Consensus quality: 168958 bases at least Q20
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 Sequencing vector: M13; 52%
Sequencing vector: plasmid; 48%
 Center project Information Center project name: H_NH0692K15 Drafting center: WIBR
 Submitted (11-JAN-2002) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. MO 63108, USA
On Jan 11, 2002 this sequence version replaced circolors
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Waterston, R.H.
 Chemistry: Dye-primer ET; 0% of reads
 Center: Washington University Genome Sequencing Center Center code: WUGSC
 Unpublished
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 Homo sapiens
 * NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
 Contact: submissions@watson.wustl
 Web site:http://genome.wustl.edu/gsc/index.shtml
 Waterston, R.H.
 The sequence of Homo sapiens clone
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1310: gap of unknown length
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 Genome Center -----
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 200 others
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AUTHORS
TITLE
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AUTHORS
 DEFINITION
ACCESSION
 Percent Similarity:
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AUTHORS
TITLE
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SOURCE
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LOCUS AC097661
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US-10-048-197-2 x AC106051
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 Align seg 1/1 to: AC106051
 Percent Similarity: 100.000
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 JOURNAL
 TITLE
 ORGANISM
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 TGGCAGGAGATTTTGTCTTTAATTATA 70873
 Quality:
 Center: Washington University
Center code: WUGSC
Web site:http://genome.wustl.c
 Direct Submission
Submitted (03-JAN-2002) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. MO 63108, USA
On Dec 21, 2001 this sequence version replaced gi:17298655.
 Waterston,R.H.

Direct Submitssion
Submitted (21-DEC-2001) Genome Sequencing Center, Washing University School of Medicine, 4444 Forest Park Parkway, MO 63108, USA
 Drafting center: WIBR
 Waterston, R.H.
 Submitted (20-007-2001) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
 169197 bp DNA linear PRI 03-JAN-
HOMO Sapiens chromosome 4 clone RP11-553E15, complete sequence.
AC097661 AC023845
AC097661.3 GI:17975439
 Direct Submission
 Waterston, R.H.
 The sequence of Homo sapiens clone Unpublished
 Waterston, R.H.
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 Eukaryota;
 Homo sapiens
 Ratio:
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 (bases 1 to 169197)
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1.000
100.000
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 Location/Qualifiers
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31106 c 29512 g
 2001 this sequence version replaced gi:17298655.
 Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 to 169197)
 Percent Identity:
 from: 1
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 Genome Center -----
 Percent Identity: 100.000
 to: 168577
 Genome Sequencing Center
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 linear PRI 03-JAN-2002
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Parkway, St.
 Louis,
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AUTHORS
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JOURNAL
REFERENCE
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AUTHORS
 COMMENT
 VERSION
KEYWORDS
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JOURNAL
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 Green, E.D.
 AC074041
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 This sequence was finished as follows unless otherwise noted: all regions were double-stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by more than one M13 subclone; and the assembly was confirmed
 CLONE LENGTH: This sequence represents the entire insert of this clone unless otherwise noted. If there are overlapping
 the Features section
 clones, the overlaps are noted
 by restriction
 Submitted (28-JUN-2001) NIH Intramural Sequencing Center, 8717 Grovemont Circle, Gaithersburg, MD 20877, USA On Jun 28, 2001 this sequence version replaced g1:11024833.
 Direct Submission
Submitted (13-JUL-2000) NIH Intramural Sequencing Center, 8717
Grovemont Circle, Gaithersburg, MD 20877, USA
3 (bases 1 to 170548)
 Ayele, K. Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Ho, S.-L., Idol, J.R., Karlins, E., Lee-Lin, S.-C., Legaspi, R., Lim, M., Maduro, Q.L., Maduro, V.B., Masiello, C., Mastrian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Prasad, A., Shevchenko, Y., Snyder, B., Stantripop, S., Thomas, J.W., Thomas, P.J., Touchman, J.W., Tsurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Zhang, L.-H. and Green, E.D.
 Direct Submission
 AC074041 170548 bp DNA linear ROD 28-0 Mus musculus chromosome 2 clone RP23-258D16 strain C57BL6/J
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 AC074041.3 GI:14573692
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 Center: NIH Intramural Sequencing Center
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 Location/Qualifiers
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 Genome Center
 in
 . If there are overlapping the beginning and end of
 to: 169197
 ROD 28-JUN-2001
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TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE

JOURNAL

COMMENT

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ORGANISM
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Quality:
Ratio:
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KEYWORDS
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US-10-048-197-2 x AC074041/rev
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Ratio: 1.000
Percent Similarity: 100.000
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Benton, J., Bilandeye, R.C., Bonnin, D., Bouck, J., Boule, S., Briava, M., Brown, E., Bonnin, D., Bouck, J., Bowle, S., Briava, M., Brown, E., Brown, M., Bryant, N.P., Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Carron, T.F., Carron, T.F., Chen, C., Chen, G., Chen, G., Chen, G., Chen, G., Chen, G., Chen, G., Chen, C., Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K., Harris, C., Hodgson, A., Hogues, M., Holloway, C., Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Jackson, L. E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L., Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Lewis, L., Li, J., Li, R., Martin, R., Martindale, A., Martinez, E., Massey, E., Mawhiney, E., McLeod, M.P., Meador, M., Mayuen, N., Noser, M., Nelecod, M.P., Meador, M., Mayuen, N., Nickerson, E., Wookenko, S., Oguh, M., Okwuonu, G., Oragunye, N., Nickerson, E., Nookenko, S., Oguh, M., Staton, I., Sodergren, E., Sonaike, T., Sparks, A., Stanley, H., Stooshtari, N., Stone, H., Shooshtari, N., Stone, H., Shooshtari, N., Stone, H., Shooshtari, N., Tangrisa, A., Stanley, H., Tangrisa, N., Tangrisa, A., Tangrisa, N., Tangrisa, N.
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Rattus norvegicus clone CH230-68A17, *** SEQUENCING IN PROGRESS
***, 75 unordered pieces.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus norvegicus
 HTG; HTGS_PHASE1.
 AC099145.2 GI:17973022
 AC099145
 Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Banks,T.,
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 Norway rat.
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a 37418 c 35891 g 45357 t
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 Submitted (09-NOV-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Dec 20, 2001 this sequence version replaced gi:16874639.
 * NOTE: Estimated insert size may differ from sequence length

* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently

* NOTE: This is a 'working draft' sequence of the pieces

* consists of 75 contigs. The true order of the pieces

* is not known and their order in this sequence record is
 findPhrapList
 Direct Submission
 Worley, k.c
 Unpublished
 Direct Submission
 arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
 (bases
 Consensus quality: 137202 bases at least Q40 Consensus quality: 145881 bases at least Q30 Consensus quality: 153638 bases at least Q30 Estimated insert size: 146753; sum-of-contigs estimation Quality coverage: 0x in Q20 bases; agarose-fp estimation quality coverage: 1.9x in Q20 bases; sum-of-contigs estimation
 Center project name: GGYQ
Center clone name: CH230-68A17
----- Summary Statistics
Assembly program: Phrap; version 0.990329First call to
 Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
 Center: Baylor College of Medicine
 Center code: BCM
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18801
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23195
23295
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 -- Genome Center
 41993:
 41893:
 Project Information
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Jwn length
bp in length
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n length
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length
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length
bp in length
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bp in
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REFERENCE
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JOURNAL
REFERENCE
AUTHORS
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ORGANISM
 ACCESSION
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Percent Similarity: 100.000
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 http://ftp.genome.washington.edu/RM/RepeatMasker.html

Center: Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
Center project Information
Center project name: L3908
Center clone name: 20_I_14
 Submitted (15-NOV-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Apr 1, 2000 this sequence version replaced gi:6554527. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
 Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 175706)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens chromosome, clone RP11-20114
 AC013798 175706 bp DNA linear HTG 01-APR-2000 Homo sapiens clone RP11-20114, WORKING DRAFT SEQUENCE, 13 unordered
 Unpublished
 human.
 AC013798.4 GI:7382144
HTG; HTGS_PHASE1; HTGS_DRAFT.
Sequencing vector: M13; M77815; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads
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138352
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139966
141535
141635
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Gaps:
Percent Identity:
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f unknown
g of 1514
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g of 1569
f unknown
g of 1922
unknown
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n length
bp in length
n length
n length
bp in length
length
length
 : 9
: 0
: 100.000
 bp in length
 in length
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 NOTE: This is a 'working draft' sequence. It currently consists of 13 contigs. The true order of the pieces is not known and their order in this sequence record is
 arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
 consensus quality: 166346 bases at least Q40 consensus quality: 169904 bases at least Q30 consensus quality: 171637 bases at least Q20 Insert size: 183000; agarose-fp Insert size: 174506; sum-of-contigs Quality coverage: 5.2 in Q20 bases; agarose-fp Quality coverage: 5.5 in Q20 bases; sum-of-contigs
 57052 6725
67257 67356:
67357 9721
 134360 134459:
 Assembly program: Phrap; version 0.960731
 97220 97319:
97320 1343
 56952 57051:
 45082
 44982 45081:
 1 1504: contig of 1504 bp in length
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4187 4286: gap of 100 bp
4287 6724: contig of 2438 bp in length
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 28008:
 34459: gap of
175706: cont
 27908: 7
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 in length
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AUTHORS
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 COMMENT
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Wheeler, J., Wu, X., Wyman, D., Ye, W.J. and Zody, M.
 Submitted (13-AUG-1999) whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On May 25, 2000 this sequence version replaced gi:7328737. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 178670)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens, clone RP11-45118
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 Unpublished
 human.
 AC009290.3 GI:8072429
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 lomo sapiens
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Sequencing vector: M13; M77815; 93% of reads
 Center project name: L1165
Center clone name: 45_I_18
 Contact: sequence_submissions@genome.wi.mit.edu
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NOTE: This is a 'working draft' sequence. It currently consists of 10 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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27096 442276: contig of 10238 bp in length
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27096 442276: contig of 15181 bp in length
42277 43376: gap of 100 bp
42277 60953: contig of 18577 bp in length
43377 60953: contig of 18577 bp in length
61054 83707: contig of 26644 bp in length
81708 83807: gap of 100 bp
81808 116924: contig of 33117 bp in length
81708 03807: gap of 100 bp
81808 116924: contig of 33117 bp in length
 83808 116924: courty - 100 bp
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VERSION
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 AUTHORS
 Ratio: 1.000 Percent Similarity: 100.000
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 Submitted (22-JAN-2001) NIH Intramural Sequencing Center, 8717 Grovemont Circle, Gaithersburg, MD 20877, USA On Jan 22, 2001 this sequence version replaced gi:11038457.
 Ayele, K. Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Brinkley, C., Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Ho, S.-L., Idol, J.R., Karlins, E., Lee-Lin, S.-Q., Legaspi, R., Lim, M., Maduro, Q.L., Maduro, V.B., Masiello, C., Mastrian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Prasad, A., Shevchenko, Y., Snyder, B., Stantripop, S., Thomas, J.W., Thomas, P.J., Tiongson, E.E., Touchman, J.W., Tsurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Zhang, L.-H. and Green, E.D.
 Submitted (20-JUL-2000) NIH Intramural Sequencing Center, 8717 Grovemont Circle, Gaithersburg, MD 20877, USA
 Direct Submission
 Green, E
 Direct Submission
 Green, E.D.
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 Unpublished
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Insert size: 192075; sum-of-contigs
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 Submitted (08-FEB-2000) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. MO 63108, USA
 2 (bases 1 to 194575) Waterston, R.H.
 web site:http://genome.wustl.edu/gsc/index.shtml
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 Direct Submission
 The sequence of Homo sapiens Unpublished
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 53467
 Jun 17,
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 Submitted (15-MAY-2000) Human Genome Sequencing Center, Depart of Molecular and Human Genetics, Baylor College of Medicine, Baylor Plaza, Houston, TX 77030, USA
On Sep 25, 2001 this sequence version replaced gi:11128156.
 Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R. Wall, R., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S., Williams, G., Williamson, A., Wleczyk, R., Wooden, S., Worley, K., Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D. Weinstock, G. and Gibbs, R.
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 Direct Submission
 Inpublished
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 HTG; HTGS_PHASE1; HTGS_DRAFT
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 (bases
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 ---- Genome Center
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AUTHORS
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204993 bp DNA line
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SEQUENCE, 26 unordered pieces.
 Unpublished
 AC024447
 Homo sapiens chromosome
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 Homo sapiens
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 Submitted (28-FEB-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Apr 11, 2000 this sequence version replaced g1:7108243.
 All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
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 NOTE: This is a 'working draft' sequence. It currently consists of 26 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
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4152 4251: gap of 100 bp
4252 6077: contig of 1826 bp in length
6078 6177: gap of 100 bp
6178 10158: contig of 3981 bp in length
 Contact: sequence_submissions@genome.wi.mit.edu
 Center: Whitehead Institute/ MIT Center for Genome Research Center code: WIBR
 Web site: http://www-seq.wi.mit.edu
 28415
32585
 19707
 10159
 16430 16529: gap of 19606: cont
28414: gap of 100 bp 10 32584: contig of 4170 bp in 32684: gap of 100 bp 10 37793: contig of 5109 bp in
 24359:
 19706:
 13540:
 10258:
 Ferreira, P., FitzHugh, W., Forrest, C., Gage, D.,
 540: gap of
16429: cont
 706: gap of 100 bp
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359: gap of 100 bp
28314: contig of 3955 bp
 258: gap of 100 bp
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contig of 3077 bp in
 in
 'n
 length
 length
 length
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JOURNAL

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 cont
o: gap of
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 0240: gap of
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 Direct Submission
Submitted (09-AUG-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA on Jan 2, 2002 this sequence version replaced g1:15135816.
 Worley, K.C.
 Unpublished
 Direct Submission
 findPhrapList
 NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 19 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Assembly program: Phrap; version 0.990329First call to
 Web site: http://www.hgsc.bcm.tmc.edu/Contact: hgsc-help@bcm.tmc.edu
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 -- Genome Center
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JOURNAL REFERENCE AUTHORS TITLE

JOURNAL

TITLE

COMMENT

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Mus musculus chromosome 4 clone RP23-184J13 map 4, WORKING DRAFT
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 Iliev, I., Johnson, R.,
 Murinae; Mus
 Nguyen, C.,
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COMMENT JOURNAL

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Contact: sequence_submissions@genome.wi.mit.edu

Center project Information

Center project Information

Center project Information

Center clone name: 184_J_13

Sequencing vector: Plasmid; n/a; 100% of reads

Chemistry: Dye-terminator Big Dye; 100% of reads

Chemistry: Dye-terminator Big Dye; 100% of reads

Assembly program: Phrap; version 0.960731

Consensus quality: 206496 bases at least Q40

Consensus quality: 20737 bases at least Q20

Insert size: 214000; agarose-fp

Quality coverage: 8.8 in Q20 bases; agarose-fp

Quality coverage: 9.1 in Q20 bases; sum-of-contigs
 Submitted (16-NOV-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
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be preserved.
 NOTE: This is a 'working draft' sequence. It currently consists of 13 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
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25496 32724: contig of 7229 bp in length
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DNA Res. 8 (5), 205-213 (2001)
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 Kaneko,T., Nakamura,Y., Wolk,C.P., Kuritz,T., Sasamoto,S., Watanabe,A., Iriguchi,M., Ishikawa,A., Kawashima,K., Kimura Kishida,Y., Kohara,M., Matsumoto,M., Matsuno,A., Muraki,A., Nakazaki,N., Shimpo,S., Sugimoto,M., Takazawa,M., Yamada,M. Yasuda,M. and Tabata,S.
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 Direct Submission
Submitted (02-MAY-2001) Takakazu Kaneko, Kazusa DNA Research
Institute, The First Laboratory for Plant Gene Research; Yana
1532-3, Kisarazu, Chiba 292-0812, Japan
 (E-mail:kaneko@kazusa.or.j
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Percent Similarity: 100.000
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Akagawa, S., Mizoguchi, H., Ando, S., Hayash
Yokoi, H., Tateishi, N., Senoh, A., Ikeda, M.
 Corynebacterium glutamicum.
Corynebacterium glutamicum
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Corynebacteriaceae;
 Novel polynucleotides
Patent: EP 1108790-A 515 20-JUN-2001;
KYOWA HAKKO KOGYO CO., LTD. (JP)
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 Quality:
 Submitted (18-OCT-2000) Crop and Soil Environmental Sciences, Virginia Tech, 350 Smyth Hall, Blacksburg, VA 24061-0404, USA Location/Qualifiers
 2 (bases 1 to 293)
Jeong,S.C., Hayes,A.J., Biyashev,R.M. and Saghai Maroof,M.A.
Direct Submission
 Jeong, S.C., Hayes, A.J., Biyashev, R.M. and Saghai Maroof, M.A. Diversity and evolution of a non-TIR-NBS sequence family that clusters to a chromosomal 'hotspot' for disease resistance genes in
 1 (bases 1 to 293)
Jeong, S.C., Hayes, A
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
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Glycine max
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KEYWORDS

VERSION ACCESSION DEFINITION

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AUTHORS

TITLE

JOURNAL

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Mitochondrion Taeniothrips inconsequens
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1 (bases 1 to 407)
Crespi,B.J., Carmean,D.A., Vawter,L. and von Dohlen,C.
Molecular Phylogenetics of Thysanoptera
Systematic Entomology (1996) In press
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Ratio:
 Submitted (10-JAN-2000) Crop and Soil Environmental Virginia Tech, Blacksburg, VA 24061-0404, USA Location/Qualifiers
 Hayes, A.J. and Saghai Maroof, M.A.
Targeted resistance gene mapping in
Theor. Appl. Genet. (2000) In press
2 (bases 1 to 312)
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 Dong W. and Chen, S.Y.
Direct Submission
Submitted (16-APR-1998) 803
Beijing 100101, P.R. China
3 (bases 1 to 519)
He,C. and Chen, S.Y.
Direct Submission
 gb_p1:AF060192
 Submitted (23 FEB-2001) Plant Biotechrof Genetics, CAS, Datun Road, Beljing Sequence update by submitter on Feb 23, 2001 this sequence version
 Glycine max putative resistance AF060192 AF325687 AF060192.2 GI:13111696
 Carmean,D.A., Crespi,B.J., Vawter,L. and von Dohlen,C. Direct Submission
Submitted (06-DEC-1995) David A. Carmean, Biological Simon Fraser University, Burnaby, BC V5AlS6, Canada Location/Qualifiers
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 Direct Submission

AL Submitted (24-MAY-1999) Da-Qiao Ding, Communications Research Laboratory, Kansai Advanced Research Center; 588-2, Iwaoka, Iwaoka-cho, Nishiku, Kobe, Hyogo 651-2401, Japan (E-mail:ding@crl.go.jp, Tel:+81-78-969-2240, Fax:+81-78-969-2249) An S. pombe gene library in which genomic DNA fragments are fused to the 5'-end of the GFP-5657 gene was constructed. S. pombe strain of those transformat with the library DNA amplified in E.coli, Plasmids were isolated, and their nucleotide sequences were determined. Petailed information and images can be seen in our web site (http://www-karc.crl.go.jp/bio/CellMagic/). Note: Only major localization is described for each clone in most cases. Because it subcellular localization of the fusion protein may differ from that subcellular localization of the fusion protein may differ from that subcellular localization of the fusion protein may differ from that subcellular localization of the fusion protein may differ from that subcellular localization of the fusion protein may differ from that subcellular localization of the fusion protein may differ from that subcellular localization of the fusion protein may differ from that subcellular localization of the fusion protein may differ from that subcellular localization of the fusion protein may differ from that subcellular localization of the fusion protein may differ from that subcellular localization of the fusion protein may differ from that subcellular localization of the fusion protein may differ from that subcellular localization of the fusion protein may differ from that subcellular localization of the fusion protein may differ from that subcellular localization of the fusion protein may differ from that subcellular localization of the fusion protein may differ from that subcellular localization subcellular local
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 Large-scale screening of intracellular protein localization in
living fission yeast cells by the use of a GFP-fusion genomic DNA
 Ding, D.Q., Tomita, Y., Yamamoto, A., Chikashige, Y., Haraguchi, T. and
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 Yamada,K., Banh,J., Banno,F., Chang,E., Dale,J.M., Goldsmith,A.D., Lee,J.M., Onodera,C.S., Quach,H.L., Tang,C., Torlumi,M., Wu,H.C., Yamamura,Y., Yu,G., Yu,S., Bowser,L., Carninci,P., Chen,H., Cheuk,R., Hayashizaki,Y., Ishida,J., Jones,T., Kamiya,A., Karlin-Neumann,G., Kawai,J., Kim,C., Koesema,E., Lam,B., Lin,J., Meyers,M.C., Miranda,M., Narusaka,M., Nguyen,M., Palm,C.J., Sakurai,T., Satou,M., Seki,M., Shinn,P., Southwick,A., Tracy,S.E., Shinozki,K., Davis,R.W., Ecker,J.R. and Theologis,A. Full Length cDNA of gene F13E7_19/AT3g02870 (GI:6728975) unpublished
 847 bp mRNA linear PLN 26. Arabidopsis thaliana putative myo-inositol monophosphatase (F13E7_19/AT3g02870) mRNA, complete cds.
 The Salk, Stanford, PGEC (SSP) Consortium members constructed and sequenced the pUNI (ORF) clones using the RAFL cDNAs: Yamada, K., Banh, J., Banno, F., Chang, E., Dale, J.M., Goldsmith, A.D., Lee, J.M., Onodera, C.S., Quach, H.L., Tang, C.C., Toriumi, M., Wu, H.C., Yamamura, Y., Yu, G., Yu, S., Bowser, L., Chen, H., Cheuk, R., Jones, T., Karlin-Neumann, G., Kim, C., Koeseman, E., Lam, B., Lin, J., Meyers, M.C., Miranda, M., Nguyen, M., Palm, C.J., Shinn, P., Southwick, A., Tracy, S.E., Davis, R.W., Ecker, J.R. and Theologis, A.
 Submitted (15-NOV-2001) Plant Gene Expression Center, 800 Buchanan Street, Albany, CA 94710, USA.
The RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL cDNA: 'RIKEN Arabidopsis Full-Length cDNA'): Seki,M., Narusaka,M., Ishida,J., Satou,M., Kanniya,A., Sakurai,T., Carninci,P., Kawai, J., Hayashizaki,Y. and Shinozaki,K.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 847)
 Yamada,K. (SSP/PGEC) and Seki, M. (RIKEN GSC) contributed equally to this work. Shinozaki,K. (RIKEN GSC) and Theologis,A. (SSP /PGEC) contributed equally to this work as PIs.
 Direct Submission
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Bown, D.P., Wilkinson, H.S. and Gatehouse, J.A.
Bifferentially regulated inhibitor-sensitive and insensitive
protease genes from the phytophagous insect pest, Helicoverpa
armigera, are members of complex multigene families
Insect Biochem. Mol. Biol. 27 (7), 625-638 (1997)
 Submitted (26-MAR-1997) D.P. Bown, University Of Durham, Sciences, Science Laboratories, South Road, Durham, DH1: Location/Qualifiers
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 Bown, D.P., Wilkinson, H.S. and Gatehouse, J.A. Differentially regulated inhibitor-sensitive and insensitive protease genes from the phytophagous insect pest, Helicoverpa armigera, are members of complex multigene families insect Blochem. Mol. Biol. 27 (7), 625-638 (1997)
 Submitted (26-MAR-1997) D.P. Boy
Sciences, Science Laboratories,
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 Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
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 H.armigera mRNA for putative serine HarS4, SR99.
 Direct Submission
 Helicoverpa armigera
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Souciet, J.L., Aiglé, M., Artiguenave, F., Blandin, G., Bolotin-Fukuhara, M., Bon, E., Brottier, P., Casaregola, S., de-Montign, J., Dujon, B., Durrens, P., Lepingle, A., Liorente, B., Malpertuy, A., Neuveglise, C., Ozier-Kalogeropoulos, O., Potier, S., Saurin, W., Tekaia, F., Toffano-Nioche, C., Wesolowski-Louvel, M., Wincker, P. and Weissenbach, J.
 1 (bases 1 to 972)
de Montigny, J., Straub, M., Potier, S., Tekaia, F., Dujon Wincker, P., Artiguenave, F. and Souciet, J.
Genomic Exploration of the Hemiascomycetous Yeasts: 8.
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Zygosaccharomyces rouxii
Zygosaccharomyces rouxii
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Saccharomycetales; Saccharomycetaceae; Zygosaccharomyces.
 Zygosaccharomyces rouxii(1)
FEBS Lett. 487 (1), 52-55 (2000)
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Patent: US 5789193-A 3 04-AUG-1998;
Location/Qualifiers
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AC043561 standard;
 Morrison H.G., McArthur A.G., Nixon J., Eakin N.Q., Kim U. Hinkle G., Holder M.E., Sogin M.L.; "Giardia: a model for ancient eukaryotic genome analysis"; Unpublished.
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12-APR-2000
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 86 LeuSerLeuIleIleSerPheLeu 93
 Submitted (06-SEP-2000) Genoscope - Centre National de Sequencage, 2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail: seqref@genoscope.cns.fr - Web: www.genoscope.cns.fr)
This STS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii, Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila, Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of Location/Qualifiers
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 Genomic Exploration of the Hemiascomycetous Yeasts: 1. A set yeast species for molecular evolution studies(1) FEBS Lett. 487 (1), 3-12 (2000)
 Direct Submission
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* sequencing reads that have not been assembled into

* contigs. Runs of N are used to separate the reads

* and the order in which they appear is completely

* arbitrary. Low-pass sequence sampling is useful for

* identifying clones that may be gene-rich and allows

* overlap relationships among clones to be deduced.

* However, it should not be assumed that this clone

* will be sequenced to completion. In the event that

* the record is updated, the accession number will
 Submitted (11-APR-2000) to the EMBL/GenBank/DDBJ databases. Josephine Bay Paul Center for Comparative Molecular Biology Marine Biological Laboratory, 7 MBL Street, Woods Hole, MA
 CGCTTGACAATCTCGGCTCTTCTG
 Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 1038)
Yamada, K., Liu, S.X., Sakano, H., Pham, P.K., Banh, J., Chung, M.K.,
Goldsmith, A.D., Lee, J.M., Quach, H.L., Tang, C., Toriumi, M., Yu, G.,
Ishida, J., Jones, T., Kamiya, A., Kariln Neumann, G., Kawai, J.,
Ishida, J., Jones, T., Kamiya, A., Kariln Neumann, G., Kawai, J.,
Kim, C., Koesema, E., Lam, B., Lin, J., Meyers, M.C., Miranda, M.,
Narusaka, M., Nguyen, M., Palm, C.J., Sakurai, T., Satou, M., Seki, M.,
Shinn, P., Southwick, A., Shinozaki, K., Davis, R.W., Ecker, J.R. and
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 G., Holder M.E., Sogin M.L.;
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 PLN 10-JUN-2001
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 The Salk, Stanford, PGEC (SSP) Consortium members carried out the sequencing and annotation of the RAFL cDNAs: Yamada,K., Liu,S.X., Sakano,H., Pham,P.K., Banh,J., Chung,M.K., Goldsmith,A.D., Lee,J.M., Quach,H.L., Tang,C.C., Toriumi,M., Yu,G., Bowset,L., Chen,H., Cheuk,R., Jones,T., Karlin Neumann,G., Kim,C., Koesema,E., Lam,B., Lin,J., Meyers,M.C., Miranda,M., Nguyen,M., Palm,C.J., Shinn,P., Southwick,A., Davis,R.W., Ecker,J.R. and Theologis,A.
 Direct Submission
Submitted (10-MAY-2001) Plant Gene Expression Center, 800 Buchanan Street, Albany, CA 94710, USA
RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL CDNAs (RAFL CDNA; 'RIKEN Arabidopsis Full-Length CDNA'): Seki,M., Narusaka,M., Ishida,J., Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J., Hayashizaki,Y. and Shinozaki,K.
 Yamada,K. (SSP/PGEC) and Seki,M. (RIKEN GSC) contributed equally this work. Shinozaki,K. (RIKEN GSC) and Theologis,A. (SSP/PGEC) contributed equally to this work as PIs.
 Yamada, K., Liu, S.X., Sakano, H., Pham, P.K., Banh, J., Chung, M.K., Goldsmith, A.D., Lee, J.M., Quach, H.L., Tang, C.C., Toriumi, M., Yu, G., Bowser, L., Carninci, P., Chen, H., Cheuk, R., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Kim, C., Koesema, E., Lam, B., Lin, J., Meyers, M.C., Miranda, M., Narusaka, M., Nguyen, M., Palm, C.J., Sakurai, T., Satou, M., Seki, M., Shinn, P., Southwick, A., Shinozaki, K., Davis, R.W., Ecker, J.R. and
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* However, it should not be assumed that this clone

* Will be sequenced to completion. In the event that
 * NOTE: This record contains 1 individual
* sequencing reads that have not been assembled into
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be generatich and allows
* identifying clones that may be generated.
 Submitted (13-APR-2000) to the EMBL/GenBank/DDBJ databases.
Josephine Bay Paul Center for Comparative Molecular Biology and Evolution,
Marine Biological Laboratory, 7 MBL Street, Woods Hole, MA 02543-1015, USA
 Giardia intestinalis
 Giardia intestinalis
 7 ArgLeuThrIleSerAlaLeuLeu
CGCTTGACAATCTCGGCTCTTCTG
 Morrison H.G., McArthur A.G., S., Holder M.E., Sogin M.L.;
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 G;
 from:
 Length:
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 LOW-PASS SEQUENCE SAMPLING
 Kim U.,
 Crocker M.C.,
 Crocker M.C.,
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 Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
 The WashU-HHMI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
 AA563389
 Tel: 314 286 1800
Fax: 314 286 1810
 WashU-HHMI Mouse EST Project
Washington University School of MedicineP
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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 Mus musculus
 AA563389.1 GI:2334854
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 4444 Forest Park Parkway, Box 8501,
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 97
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| AQ313383 RPC111-102020.TV RP
| AZ301770 AF-E8R Resistance 9
| AQ406823 HS_5092_B1_B04_Sp6E
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    ACCESSION

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIXEN), Genomic Sciences Center (GSC); 1-7-22 Subhiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170) URL:http://hgp.gsc.riken.go.jp/, Clones are derived from the chimpanzee BAC library RPCI-43 This BAC end was generated during the R&D process and may have higher chance payurers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fujlyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fujlyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
BAC end sequences of Library RPCI-43
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
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GSS; GSS (genome survey sequence).
Pan troglodytes male lymphocytes DNA, clone_lib:RPCI-43 Chimpanzee
Male BAC Library clone:RP43-011C03.TJ.
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R.Site 1 : ECORI
R.Site 2 : ECORI.
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/clone_lib="RPCI-43 Chimpanzee Male BAC Library"
87 c 99 g 249 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Pan troglodytes"
/db_xref="taxon:9598"
/clone="RP43-011C03.TJ"
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                                        LOCUS B1655178
                    DEFINITION
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US-10-048-197-2 x AI049267
                                                                                              seq_name: gb_est2:BI655178
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mRNA sequence
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Fax: 314 286 1810
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B1655178 768 bp mRNA linear EST 12-SEP-2001 603280984F1 NIH_CGAP_Mam4 Mus musculus cDNA clone IMAGE:5325357 5',
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. L/
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                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:10090"
/clone="TMAGE:1432450"
/clone_lib="Sugano mouse kidney mkia"
/sex="female"
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Gaps: 0
Percent Identity: 100.000
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Brassica oleracea.

Brassica oleracea.

Brassica oleracea

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Eukaryota; Magnollophyta; eudlootyledons; core eudicots;

Spermatophyta; Magnollophyta; eudlootyledons; core eudicots;

Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.

1 (bases 1 to 776)

Town,C.D., Van Aken,S., Utterback,T. and Fraser,C.M.
                                                                                                                                                                                                                                                                                 BH473529 776 bp DNA linear GSS 13-DEC-2001
BOGDF02TF BOGD Brassica oleracea genomic clone BOGDF02, DNA
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Plate: LLAM11825 row: g column: 22
High quality sequence stop: 760.
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (1999)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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/clone_lib="NIH_CGAP_Mam4"
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/lab_host="DH10B"
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                                                                                                                                     WashU Xenopus EST project, 1999
Unpublished (1999)
Contact: Sandy Clifton, Ph.D.
WashU Xenopus EST project, 1999
WashIngton University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Lou
Tel: 314 286 1810
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gb_est2:BE679654
Library constructed by Bruce Blumberg
Library normalized by Jihwan Song
DNA Sequencing by: Washington University Genome Sequencing
Clone distribution: Xenopus clone distribution information
this library can be found through Research Genetics, visit t
web page at: http://www.resgen.com/ Please reference the id
                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 107)
Clifton,S., Johnson,S.L., Blumberg,B., Song,J., Hillier,L., Pape,D.,
    Martin,J., Wylie,T., Underwood,K., Theising,B., Bowers,Y., Person
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               df51e06.yl Xenopus laevis unfertilized egg cDNA library Xenopus laevis cDNA clone IMAGE:3742882 5', mRNA sequence.
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African clawed frog.
Xenopus laevis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Whole genome shotgun sequencing of Brassica oleracea Unpublished (2001) Other_GSSs: BOGDF02TR
                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Class: sheared ends.
                                                                                                                                                                                                                                                                                                 ,B., Gibbons,M., Harvey,N., Ritter,E., Jackson,Y., McCann,R., Waterston,R. and Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BE679654.1 GI:10062553
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: cdtown@tigr.org
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                                                                                                                    Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                   197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Vector: pHOS1; Site_1: BstXI; 2-3 kb sheared
genomic DNA inserted into pHOS1 using BstXI linkers"
1 142 c 218 g 219 t
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/strain="TO1000DH3"
/db_xref="taxon:3712"
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                                                                                                                                                                                                                                                                                                                                                                                                                        Euteleostomi;
; Pipidae;
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FEATURES
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US-10-048-197-2 x BE679654/rev
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                                                                                                                                                                                                                                      Dept. of Pathobiology, College of Veterinary Medicine University of Florida 2015 SW 23rd Avenue, Bidg 1017, Gainesville, FL 32611, Tel: 352 392 4700
Fax: 352 392 9704
                                                                                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 198)
Carlton, J.M.-R. and Dame, J.B.
The Plasmodium vivax and P. berghei gene sequence tag projects
Parasitol. Today 16 (10), 409 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Plasmodium vivax
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                       Class: shotgun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GSS
                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Dame
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           malaria parasite P. vivax.
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238PvG04 Pv MBN #26/#27 (amplified once) Plasmodium vivax genomic
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Seq primer: -40RP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               , DNA sequence.
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                                                                                                                                                                il: damej@mail.vetmed.ufl.edu
primer: M13(-20) forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            32
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a 17 c
/strain="Belem"
                         ∕organism="Plasmodium vivax"
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/clone_lib="Xenopus laevis unfertilized egg cDNA library"
/tissue_type="unfertilized egg"
/lab_host="Top-10_F/"
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/db_xref="taxon:8355"
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SOURCE

High quality sequence stop: 201

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LOCUS AZ470169
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US-10-048-197-2 x AZ567757/rev
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Ratio: 1.000
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Tel: 801 585 5606
Fax: 801 585 7177
Email: dduun@epnetics.utah.edu
Insert Length: 10000 Std Error: 0.
Plate: 0284 row: B column: 12
Seq primer: CGTOTANAACGACGGCCAGT
Class: plasmid ends
                                                                                                                                                                                                                                                                           plasmid inserts
Unpublished (2000)
Contact: Robert B.
                                                                                                                                                                                                                                                                                                                                               Mouse whole genome sca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               University of Utah Genome Center University of Utah
                                                                                                                                                                                                                                                                                                                                                                                      Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
                                                                                                                                                                              84112,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus (bases 1 to 201)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Vector: Lambda ZAP II (Stratagene); individual clones excised into phagemid pBluescript; Site_1: EcoR I; Site_2: EcoR I; Genomic DNA was prepared from asynchronous blood stage forms of the Belem line of P. vivax grown in squirrel monkeys. Parasitized erythrocytes were purified from contaminating host leukocytes by filtration of ADP activated blood through acid-washed glass beads and Whatman CFI1 cellulose columns by gravity filtration. Purified DNA was digested with mung bean nuclease in the presence of 42.5% formamide at 50oc as described (Galinski, M. et al. 1992. Cell 69,1213-1226; Vernick, K.D. et al. 1988. N.A.R. 16, 6883-6896). Eco RI linkers were added and the constructs ligated into Lambda ZAP III. P. vivax Belem was originally isolated from a patient in Belem, Brazil 1980 by Mercia de Arruda, adapted to Saimiri monkeys by Jurg Gysin, and maintained since 1983 in squirrel monkeys."
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/clone_lib="Pv MBN #26/#27 (amplified once)"
/dev_stage="asexual blood forms"
/lab_host="Saimiri boliviensis"
                                                                                                                                                                                                                                                                                                                                       scaffolding with paired end reads from 10kb
                                                                                                                                                                                                Polymers Research Bldg.,
                                                                                                                                                                                                                                                                              Weiss
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US-10-048-197-2 x AZ470169/rev
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Ratio: 1.000
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                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammaila; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 22 1 (bases 1 to 202)

Ex Konno, H., Aizawa, K., Akahira, S., Akiyama, J., Carninci, P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Hirozane, T., Hori, F., Ishii, Y., Ishikawa, T., Itoh, M., Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N., Kojima, Y., Koya, S., Kusakabe, M., C., Kawai, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y., Watsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Sato, K., Shibata, K., Shibata, V., Shigemoto, Y., Saito, H., Sano, M., Sato, K., Shibata, K., Shibata, Y., Shiraki, T., Sogabe, Y., Sugahara, Y., Suzuki, H., Takahashi, F., Tateno, M., Tominaga, N., Tsunoda, Y., Watahiki, A., Watanabe, S., Yamamura, T., Yasunishi, A., Yokota, T., Yoshiki, A., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AV331944 RIKEN full-length enriched, adult male medulla oblongata Musmusculus cDNA clone 6330528C24 3', mRNA sequence.
                              RIKEN Mouse ESTs (Konno, H., et al. 1999)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AV331944.1 GI:6371996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AV331944
Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with 74 DNA polymerase and 74 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMDA2 (gl14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XI10-Gold (Stratagene) cells and selected for ampicillin resistance."
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/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Laboratory Mouse DNA Resource
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/db_xref="taxon:10090"
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Gaps: 0
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alignment_block:
US-10-048-197-2 x AV331944/rev
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seq_name: gb_est2:BE826421
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Ratio: 1.000
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                                                                       103 LeuSerPheTyrLeuThrAlaLys 110
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Carninci,P. and Hayashizaki,Y. High-efficiency full-length cDNA cloning. Methods Enzymol. 303.
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URL:http://genome.gsc.riken.go.jp/,
Sasaki.N., Izawa.M., Watahiki.M., Ozawa.K., Tanaka.T.,
Matsuura.S., Carninci.P., Muramatsu.M., Okazaki.Y. and
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
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Fax: 81-45-503-9216
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/lab_host="DH10B"
/note="Site_1: Sall; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory.
                                                                                                                                                                                                                                                                                                                                                                                                                                       from Lambda FLC
BamHI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Mus musculus"
/strain="C57BL/6J"
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/dev_stage="adult"
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Hayashizaki
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DEFINITION
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LOCUS AI231241
                                                                                                                                                                  seq_name: gb_est1:AI231241
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US-10-048-197-2 x BE826421
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Ratio: 1.000
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AUTHORS
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LOCUS BFR26471
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                                                                                                                                                                                                                                                   ArgLeuThrIleSerAlaLeuLeu 14
                                                                                                                                                                                                                     CGGCTTACCATCTCGGCTCTTCTC 189
210 bp EST227929 Normalized rat embryo, REMDH53 3' end, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Quality:
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-Sp,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=QV4-EN0040-250
500-227-cl1&t3=2000-05-25&t4=1)
Seq primer: puc 18 forward
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Fax: +55-11-2707001
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Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequence tags
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/db_xref="taxon:9606"
/clone_lib="EN0040"
/dev_stage="Adult"
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LOCUS BH530215
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US-10-048-197-2 x AI231241
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            TIGR
9712 Medical Center Drive,
Tel: 301-338-3523
Fax: 301-838-0208
                                                                                                                                                                                                                                                                              Brassica oleracea.

Brassica oleracea

Brassica oleracea

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
                                                                                                                                                1 (bases 1 to 216)
Town, C.D., Van Aken,S., Utterback,T. and Fraser,C.M.
Whole genome shotgun sequencing of Brassica oleracea
Unpublished (2001)
Other GSSS: BOHBISOTR
                                                                                                                                       Contact: Chris Town
                                                                                                                                                                                                                                                                                                                                                                                                                                                               GSS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence.
BH530215
BH530215.1 GI:17746359
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Contact: Lee, NH
The Institute for Genomic Research
9712, Medical Center Drive, Rockvil
Tel: (301)-838-3529
Fax: (301)-838-0208
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Rattus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Seq primer: M13-21.
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Lee, N.H., Glodek, A., Chandra, I., Mason, T.M.,

Kerlavage, A.R. and Adams, M.D.

Rat Genome Project: Generation of a Rat EST (
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AI231241.1
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/Ob_xref="ATCC (inhost):2037375"
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/Ob_xref="taxon:10118"
/Clone="RENDH53"
/Clone_lib="Normalized rat embryo, Bento Soares"
/Clone_lib="Normalized rat embryo, Bento B
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Gaps: 0
Percent Identity: 100.000
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                                                                           Rockville,
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                                                                     MD 20850, USA.
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VERSION
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LOCUS BJ093812
DEFINITION BJ093812 NIBI
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US-10-048-197-2 x BH530215/rev
                                                                                                                          BASE COUNT
ORIGIN
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Ratio: 1.000
Percent Similarity: 100.000
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  Ouality: 8.00
Ratio: 1.000
Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 218 bp mRNA linear EST 12-DEC-2001 BJ093812 NIBB Mochil normalized xenopus early gastrula library xenopus laevis cDNA clone XL143j12 5', mRNA sequence. BJ093812 BJ093812.1 GI:17593552
                                                                                                                                                                                                                                                                                                                                                           Center For Genetic Resource Information National Institute of Genetics 1111 Yata, Mishima, Shizuoka 411-8540, Japan Tel: 81-559-81-6856 Fax: 81-559-81-6855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eamphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA is from a doubled haploid provided by Tom Osborn. Seq primer: TF Class: sheared ends.
                                                                                                                                                                                                                                                                                                                    Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Tadasu Shin-i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Expressed genes in X. laevis embryo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /Clone_lib="BOHB"
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/note="Vector: pHOS1; Site_1: BstXI; 2-3 kb sheared
/note="Vector: pHOS1; Site_1: BstXI; 2-3 kb sheared
genomic DNA inserted into pHOS1 using BstXI linkers"
18 c 50 g 79 t
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46 c 58 g 56 t
                                                                                                                                                                                                                                        /organism="Xenopus laevis"
/db_xref="taxon:8355"
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                                                                                                                                                                                                                      /clone_lib="NIBB Mochii normalized Xenopus early gastrula
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Pipidae;
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AUTHORS
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US-10-048-197-2 x AA480791/rev
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US-10-048-197-2 x BJ093812/rev
seq_name: gb_gss:AZ782323
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LOCUS AA480791
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Ratio: 1.000
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                                        131 ATTTCTTCTCGGTTTGGGTCTGCT 108
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                                                        IleSerSerArgPheGlySerAla 59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 243)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anat
Tumor Gene Index_
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                      /note-"Vector: pAMP10; mRNA made from invasive kidney tumor, CDNA made by oligo-dT priming. Non-directionally cloned. Size-selected on agarose gel, average insert size 600 bp. Reference: Krizman et al. (1996) Cancer Research 56:5380-5383."
                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="IMAGE:911151"
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/lab_host="DH10B"
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/db_xref="taxon:9606"
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    Align seg 1/1 to reverse of: AZ782323

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US-10-048-197-2 x AZ782323/rev
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AUTHORS
                                                                                                                                 Percent Similarity:
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LOCUS AZ782323
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                                                                                                                                                                                 Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: (
Plate: 0022 row: G column: 01
Seq primer: CACACAGGAAACAGCTATGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         High quality sequence stop: 279.
Location/Qualifiers
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Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         University of Utah Genome Center University of Utah
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                         Ratio:
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                                                                                                                                                                                                                                                                                                                                                                                                                   (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114 [gb]AF129(72.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and nurified The sheared adaptors of prepared menus pure constants.
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                                                                                                                                                                                                                                                                                          purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

46 c 52 g 53 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Biomedical Polymers Research Bldg., 20 S. 2030 E.,
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/strain="C57BL/6J"
/db_xref="taxon:10090"
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Percent Identity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTGAGTTTGATTATTTCCTTCCTT 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0027 row: G column: 12
Seq primer: CACACAGGAAACAGCTATGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             High quality sequence stop: 282.
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Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (2000)
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282 bp DNA linear GSS 16-FEB-200
2M0027G12R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0027G12 R, DNA sequence.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                       99
                                                                                                           (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pND42 (gil4732114|gb|AFI2972.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vactor DNA and transformed into
  adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

94 c 80 g 42 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:10090"
/clone="UUGC2M0027G12"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
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/strain="C57BL/6J"
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alignment\_scores:
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US-10-048-197-2 x AZ784705/rev
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Ratio: 1.000
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Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                          7 ArgLeuThrIleSerAlaLeuLeu 14
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Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.
xf11e07 x1 NCI_CGAP_Kid8 Homo sapiens cDNA clone IMAGE:2617764 3' similar to contains Alu repetitive element;contains element MSR1
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l: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/
Location/Qualifiers
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/clone="LCL091bil_r"
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/clone_lib="Chlamydomonas reinhardtii 5% to 0.04% CO2"
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/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
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                                                                     AUTHORS
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                                                                                                                                                                                                                                  BB477818 RIKEN full-length enriched, 13 musculus cDNA clone D330027A14 3', mRNA BB477818
                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 301)
Konno, H., Alzawa, K., Akahira, S., Akiyama, J., Arakawa, T., Carninci
                                                                                                                                                                                             EST.
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CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
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AW148390
AW148390.1 GI:6196211
EST.
,P., Endo,T., Fukuda,S., Fukunishi,Y., Hara,A., Hayatsu,
Hirozane,T., Hori,F., Ishii,Y., Ishikawa,J., Ishikawa,T.
Izawa,M., Kadota,K., Kagawa,I., Kai,C., Kawai,J., Kikuch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D.,
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
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1 (bases 1 to 301)
                                                                                                                                                    Mus musculus
                                                                                                                                                                   house mouse.
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Organ: kidney; Vector: pCMV-SPORT6; Site_1: Sall; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.2 kb. Life Technologies catalog #: 11524-014"
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                                           Hayatsu, N.,
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URL:http://genome.gsc.riken.go.jp/
Carninci.p., Nishiyama.Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J., Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ,Y. and Hayashizaki,Y.
Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (2000)
Contact: Yoshihide Hayashizaki
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Matsuyama, T., Miki, R., Mizuno, Y., Makamira, M., Oda, H., Okazaki, Y.
Ono, T., Owa, C., Saito, H., Sakai, C., Sato, K., Shibata, K., Shibata, Y.
Y., Shigemoto, Y., Shinagawa, A., Shiraki, T., Sogabara, Y., Sugahara, Y.
Suzuki, H., Yuzuki, H., Tagawa, A., Takahashi, F., Tominaga, N., Toya, Yano, R., Yasunishi, A., Watahabe, S., Yamamura, T., Yamanaka, I.
Yano, R., Yasunishi, A., Yokota, T., Yoshida, K., Yoshiki, A., Watamabe, S., Yamamura, T., Yamanaka, I., M., Muramatsu, M., and Hayashizaki, Y.
PIKEN Monrae Ecte (Yorno, U.)
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Tel: 81-45-503-9222
Fax: 81-45-503-9216
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/dev_stage="13 days (
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/db_xref="taxon:10090"
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LOCUS AL582559
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 316)

Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

Full-length cDNA libraries and normalization
                                                                                                                                                                                                                      AL582559 LTI_NFL010_BC2 prime, mRNA sequence.
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BJ029356
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Expressed genes in X. laevis embryo Unpublished (2001) Contact: Tadasu Shin-i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Xenopodinae; xenopus.

1 (bases 1 to 306)

Kitayama,A., Terasaka,C., Mochii,M., Ueno,N., Shin-i,T. and Kohara
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Xenopus laevis
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/dev_stage="stage 15"
56 c 83 g 80 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="NIBB Mochii normalized Xenopus neurula
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/db_xref="taxon:8355"
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Identity: 100.000
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FEATURES

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BASE COUNT ORIGIN

Align seg 1/1

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US-10-048-197-2 x AL582559
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LOCUS BE648930
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Ratio: 1.000
Percent Similarity: 100.000
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CDNA Library Preparation: M.B. Soares Lab Clone distribution: Researchers may obtain BMAP CDNA clones from RESEARCH GENETICS. It should be noted that Bento Soares is generating a small number of additional specialized non-redundant arrays of BMAP cDNAs whose availability will be considered under appropriate and limited
                                                                                                                                                                                                                                  Contact: Chin, H
National Institute of Mental Health
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 342)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 UI-M-BH2.3-aoi-f-07-0-UI.rl NIH_BMAP_M_S3.3 Mus musculus cDNA clone UI-M-BH2.3-aoi-f-07-0-UI 5', mRNA sequence.
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Email: segref@genoscope.cns.fr, Web :
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Contact: Genoscope
                                                                                                                                  Email: mEST@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                       Genome Res. 6 (9),
                                                                                                                                                                                                                                                                                                                                                                 discovery
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus
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301 443 9890
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/note="Vector: pcMVSPORT 6; Site_1: NotI; list strand cDNA
/note="Vector: pcMVSPORT 6; Site_1: NotI; list strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pcMVSPORT 6
/vector. Library was normalized. Library was constructed by
Life Technologies. Contact: Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax: (1) 301 610 8371
Email: fliang@lifetech.com URL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  http://fulllength.invitrogen.com"
101 c 77 g 68 t
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/clone="CSODL010YK13"
/clone_11b="LTI_NFL010_BC2"
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/db_xref="taxon:9606"
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Gaps: 0
Percent Identity: 100.000
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US-10-048-197-2 x BE648930
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Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Quality:
                                                                                                                                                                                                                             1 (bases 1 to 344)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      African clawed frog.
Xenopus laevis
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BG513403
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Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                Ratio:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1.000
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/clone="UI_M-BH2.3-aoi-f-07-0-UI"
/clone_1ib="NIH_BMAP_M_S3.3"
/dev_stage="27-32 days"
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Gaps: 0
Percent Identity: 100.000
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                                                                                                                                                                                                                                   Genome Anatomy Project (CGAP),
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LOCUS BH113823
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US-10-048-197-2 x BG513403/rev
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Ratio: 1.000
Percent Similarity: 100.000
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                                                                                                                                                                                              Unpublished (1999)
Other_GSS: RPCI-24-252K17.TJ
Other_GSS: RPCI-24-252K17.TJ
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MC
Tel: 301 838 0200
Fax: 301 838 0208
                   Clones are derived from the mouse BAC library RPCI-24. For BAC library availability, please contact Pieter de Jong (pdejong@mail.cho.org). Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC end page: http://www.tigr.org/tdb/bbac_ends/mouse/bac_end_intro.html Plate: 252 row: K column: 17
Seq primer: T7
                                                                                                                                                                                                                                                                                                                                                                                                 Zhao, S., Nierman, W., Malek, J., Shatsman, S., Ak
Tsegaye, G., Geer, K., Krol, M., Shvartsbeyn, A.,
Russell, D., de Jong, P. and Fraser, C.M.
Mouse BAC End Sequences from Library RPCI-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus (bases 1 to 350)
                                                                                                                                                                           Email: szhao@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA sequence.
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/note="Organ: lung; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2.6 kb. Constructed by Life
Technologies. Note: This is a Xenopus Gene Collection (XGC)
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/db_xxef="taxon:8355"
/clone="IMAGE:4632979"
/clone_lib="NICHD XGC Lul"
/dev_stage="adult"
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Gaps: 0
Percent Identity: 100.000
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mic clone RPCI-24-252K17
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US-10-048-197-2 x BH113823/rev
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JOURNAL
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Ratio: 1.000
Percent Similarity: 100.000
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                                                                                                       PCR PRIMERS
FORWARD: T3
BACKWARD: T7PL
                                                                                                                                                                                                                                                                                                                                      Contact: Blaxter ML
Institute of Cell, Animal and Population Biology
University of Edinburgh
Ashworth Labs, King's Buildings, West Mains Road, Edinburgh, EH9
                                                                               Plate: 42 row:
                                                                                                                                                                                  The library was prepared by Richard Grencis, Manchester University, Manchester. Sequencing was performed by the Pathogen Sequencing Unit, Sanger Centre, Cambridge, UK (Neil Hall, Mike Quail & Bart
                                                                                                                                                                                                                                                                                  Tel: +44 131 650 6760 Fax: +44 131 670 5450
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Blaxter,M.L., Parkinson,J., Whitton,C., Daub,J., Guiliano,D.,
N., Quayle,M. and Barrell,B.
Edinburgh University/Sanger Centre Nematode EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BM277543 353 bp mRNA linear EST 20-DEC-2001 Tm_ad_42B03 SKPL Trichuris muris (parasitic nematode) mixed adult Trichuris muris cDNA clone Tm_ad_42B03 5' similar to gb|AAC02985.2| (AF038554) density regulated protein drpl - Homo sapiens, mRNA
                                                                                                                                                                                                                                                             Email: mark.blaxter@ed.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Nematoda; Enoplea; Trichocephalida; Trichuridae
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primer: SKPL
/h quality sequence stop: 278.
Location/Qualifiers
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/note="Vector: pTARBAC1; Site_1: BamH1; Site_2: BamH1;
/note="Vector: pTARBAC1; Site_1: BamH1; Site_2: BamH1,
RPCI-24 Mouse BAC Library produced by Pieter de Jong. The
library was cloned in the pTARBAC1 cloning vector at the
BamH1 sites using MboI partially digested male C57BL/6J
DNA."
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/clone="RPCI-24-252K17"
/clone_lib="RPCI-24"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /strain="C57BL/6J"
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US-10-048-197-2 x BM277543/rev
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LOCUS BH033149
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Ratio: 1.000
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                                                                                                                                                                                                                 Email: szhao@tigr.org

Clones are derived from the mouse BAC library RPCI-24. For BAC library availability, please contact Pieter de Jong (pdeJong@mail.cho.org). Clones may be purchased from BACPAC Resources (http://www.chorl.org/bacpac/orderingframe.htm). BAC page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html plate: 294 row: H column: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
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358 bp DNA linear GSS 17-JUL-2001
RPCI-24-294H20.TV RPCI-24 Mus musculus genomic clone RPCI-24-294H20
                                                                                                                                                                                                                                                                                                                                                                                            The Institute for Genomic Research 9712 Medical Center Dr., Rockville, Tel: 301 838 0200 Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zhao,S., Nierman,W., Malek,J., Shatsman,S., Ak
Tsegaye,G., Geer,K., Krol,M., Shvartsbeyn,A.,
Russell,D., de Jong,P. and Fraser,C.M.
Mouse BAC End Sequences from Library RPCI-24
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                                                                                                                                                                           Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1999)
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/clone_lib="RPCI-24"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Vector: Lambda Zap II; Site_1: EcoRI (5'end); Site_2: XhoI (3'end); Trichuris muris is a menatode parasite of rodents related to the human whipworm Trichuris trichiura. The library was constructed from Trichuris muris adults (Edinburgh 'E' strain) maintained in mice, and was provided by Dr. Richard Grencis, University of Manchester."
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/clone="Tm_ad_42803"
/clone_lib="Trichuris muris (parasitic nematode) mixed adult"
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FEATURES

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US-10-048-197-2 x BH033149/rev
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Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: szhao@tigr.org

Clones are derived from the mouse BAC library RPCI-24. For BAC Library availability, please contact Pieter de Jong (pdejong@mail.cho.org). Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html Plate: 228 row: C column: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zhao, S., Nierman, W., Malek, J., Shatsman, S., Al
Tsegaye, G., Geer, K., Krol, M., Shvartsbeyn, A.,
Russell, D., de Jong, P. and Fraser, C.M.
Mouse BAC End Sequences from Library RPCI-24
Unpublished (1999)
Other_GSSs: RPCI-24-228C8.TJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The Institute for Genomic Research 9712 Medical Center Dr., Rockville, Tel: 301 838 0200 Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seq primer: T7
Class: BAC ends
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                                                                                                                                                                                                               /organism="Mus musculus"
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/clone="RPCI-24-228C8"
/clone_lib="RPCI-24"
/sex="Male"
/cell_type="Spleen/Brain"
/note="Vector: pTARBAC1; Site_1: BamH1; Site_2: BamH1;
/note="Vector: pTARBAC1; Site_1: BamH1; Site_2: BamH1;
/note="Vector: pTARBAC1; Site_1: BamH1; Site_2: BamH1;
/note="Vector: pTARBAC1 Site_2: BamH1; Site_2: BamH1;
/note="Vector: pTARBAC1 Site_2: BamH1; Site_2:
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FEATURES
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US-10-048-197-2 x BH072663
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                                                                                                                                                                                                                                                                                                                                                                                                                         The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to identify it as a clone from the normalized brain stems library cDNA Library Preparation: M.B. Soares Lab Clone distribution: NIH BMAP cDNA clones will be made available by the means that is soon to be determined. When NIH determines the means for distribution of the BMAP cDNA clones, this record will be updated accordingly when that means is determined.
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Ratio:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: mEST@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6001 Executive Blvd. Room 20892-9643, USA
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6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
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97044477
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    /clone_lib="NIH_BMAP_M_S3.3"
/dev_stage="27-32 days"
/lab_host="pH10B (Life Technologies)"
/lab_host="pH10B (Life Technologies)"
/lab_host="pH73D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The
NIH_BWAP_M_S3.3 library is a subtracted library of a
series, ultimately derived from a mixture of individually
tagged normalized libraries from ten regions of the mouse
brain (cerebellum, brain stems, olfactory bulbs,
hypothalamus, cortex, amygdala, basal ganglia, pineal
gland, striatum, hipoccampus) after a series of
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301 443 9890
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/clone="UI-M-BH2.3-aoi-f-07-0-UI"
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/strain="C57BL/6J"
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US-10-048-197-2 x AW121899/rev
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/clone_lib="Resistance gene analog.sequences of soybean
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Align seg 1/1 to reverse of: AW121899
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                                                                                                                                                                                 Contact: Young Nevin D
Department of Plant Pathology
University of Minnesota
495 Borlaug Hall, 1991 Upper Buford Circle, St. Paul MN
Tel: 612 625 2225
Fax: 612 625 9728
Email: nevinyetc.umn.edu
nonTIR-NBS-LRR RGA sequence of soybean on linkage group
                                                                                                                                               Class: RFLP probe.
                                                                                                                                                                           Seq primer: M13F
                                                                                                                                                                                                                                                                                                                                                                                                                                              Penuela,S. and Young,N.D.
Resistance gene analog se
(nonTIR-NBS-LRR type)
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papillonoideae; Phaseoleae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AF-F4F Resistance gene analog sequences of soybean type) similar to AF060192. Glycine max genomic, DNA AZ301765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AZ301765.1 GI:9886539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (bases 1 to 371)
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The subtracted library (NIH_BMAP_M_S2, NIH_BMAP_M_S1.

The subtracted library (NIH_BMAP_M_S3.3) was constructed as follows: PCRamplified CDNA inserts from NIH_BMAP_M_S1.

clones from which 3' ESTs had been derived was used as a driver in a hybridization with the NIH_BMAP_M_S2 library in the form of single-stranded circles. The remaining single-stranded circles (subtracted library) was purified by hydroxyapatite column chromatography, converted to double-stranded circles and electroporated into DH10B bacteria (LifeTechnologies) to generate the NIH_BMAP_M_S3.3 library. This procedure has been previously described (Bonaldo, Lennon and Soares, Genome Research 6:791-806, 1996)

"NAC 1'TRANTU WAND W C2.3
/organism="Glycine max"
/cultivar="Faribault"
/db_xref="taxon:3847"
                                                                              1. .371
                                                                                                                   Location/Qualifiers
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1.000
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TAG_SEQ=TCATT"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   371 bp
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SOURCE
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Ratio: 1.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
                                                                                                                                                                                                                                                                                                                                   Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error:
Plate: 0519 row: H column: 08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                     High quality sequence stop: 376.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                Seq primer: CACACAGGAAACAGCTATGACC
                                                                                                                                                                                                                                                                                                                                                                                                                 Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         plasmid inserts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mouse whole genome scaffolding with paired end reads from 10kb
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Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus
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/note="Vector: pCR2.1-TOPO; Site_1: EcoRI; Soybean genomic DNA (cv. Faribault) was amplified by PCR with primers corresponding to the 'P-loop' and the region preceding the 'GLPLA' motif of the nucleotide-binding site (NBS) of soybean GenBank accession AF060192. PCR products of approximately 450 bp were cloned into pCR2.1-TOPO vector, and sequenced with M13 universal primers."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
                                                                                                                  /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0519H08"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (nonTIR-NBS-LRR type) similar to AF060192."
/tissue_type="cotyledon leaves"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
                                                                          /sex="Male"
                                                                                              /clone_lib="Mouse 10kb plasmid UUGC1M library"
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LOCUS BB816077
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Akimura, T., Arakawa, T., Carninci, P., Furuno, M., Hanagaki, T.,
Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Imotani, K., Ishii,
Y., Ito, M., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Matsuyama, T.,
Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Okazaki, Y., Okido, T.,
Saito, R., Sakai, C., Sakai, K., Sakazume, M., Sasaki, D., Sato, K.,
Saito, R., Shiradawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagawa
A., Takahashi, F., Takaku-akahira, S., Tanaka, T., Tomaru, A., Toya, T.,
Watahiki, A., Yasunishi, A., Muramatsu, M., and Hayashizaki, Y.,
Watahiki, A., Yasunishi, A., Muramatsu, M., and Hayashizaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BB816077 RIKEN full-length enriched, lung RCB-0558 LLC cDNA Mus musculus cDNA clone G730032I23 3', mRNA sequence.
Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., II.
,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
                                                                                                                                                                                                                                                                                                         Laboratory for Genome Exploration Research Group, RIKEN Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
                                                                                                                                                                                                            1-7-22 Suehiro-cho,
Tel: 81-45-503-9222
Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (2001)
Contact: Yoshihide Hayashizaki
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura, T., et al
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     house mouse.
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                                                                                                           Shibata, K., Itoh
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SOURCE

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LOCUS AA720873
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US-10-048-197-2 x BB816077
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CysValSerThrGlyAsnValAla 29
              cDNA Library Preparation: Stratagene, Inc. cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 2417 Std Error: 0.00
                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                      Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 386) NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
                                                                                                                                                                                    Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                               Unpublished (1997)
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AA720873.1 GI:2737008
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             genes. Genome Res. . 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   further details. e mouse tissues.
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/db_xref="taxon:10090"
/clone="6730032123"
/clone_lib="RIKEN full-length enriched, lung RCB-0558 LLC
cDNA"
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-40m13 fwd. ET from Amersham
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Gaps: 0
Percent Identity: 100.000
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Homo
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JOURNAL COMMENT
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US-10-048-197-2 x AA720873
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Ratio: 1.000
Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                        Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D., Dav
Ph.D., Gerald Marti, M.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M.
Bonaldo, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
Bonaldo, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
CDNA Sequencing by: Washington University Genome Sequencing the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                      www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 1594 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 304.
Location/Qualifiers
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National Cancer Institute, Cancer Genome Anat
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AAR7-1998

AA872067

AAR7-1998

AA872067

AAR7-1998

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence.
AA872067
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Location/Qualifiers
/clone="IMAGE:1336280"
/clone_lib="NCI_CGAP_GCB1"
                                                                                    /organism="Homo sapiens"
/db xref="taxon:9606"
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/clone_lib="NCI_CGAP_SS1"
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/db_xref="taxon:9606"
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Gaps: 0
Percent Identity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                    Sequencing Center information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   David Allman,
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/tissue\_type="germinal center

B cell"

/lab\_host-"DH10B"

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ACCESSION
VERSION
KEYWORDS
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US-10-048-197-2 x AA872067/rev
alignment_scores:
    Quality:
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ORIGIN
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ORIGIN
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LOCUS BJ069087
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Ratio: 1.000
Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gb_est2:BJ069087
                                                                                                                                                                                                                                                                                   Center For Genetic Resource Information National Institute of Genetics 1111 Yata, Mishima, Shizuoka 411-8540, Japan Tel: 81-559-81-6855 Fax: 81-559-81-6855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BJ069087 NIBB Mochii normalized Xenopus tailbud library Xenopus Laevis cDNA clone XL051116 5', mRNA sequence.
                                                                                                                                                                                                                                              Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                              Contact: Tadasu
                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (2001
                                                                                                                                                                                                                                                                                                                                                                                                               Expressed genes in X. laevis embryo
                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 397)
Kitayama, A., Terasaka, C., Mochii, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Xenopus laevis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           African clawed frog.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          constructed by Bento Soares and M. Fatima Bonaldo."
                                                                                     /dev_stage="stage 25"
81 c 105 g
                                                                                                                                                                           /clone="XL051116"
                                                                                                                                                                                              /organism="Xenopus laevis"
/db_xref="taxon:8355"
                                                                                                                           /tissue_type="whole embryo"
                                                                                                                                                             /clone_lib="NIBB Mochii normalized Xenopus tailbud
   8.00
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Gaps: 0
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6
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REFERENCE
AUTHORS
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US-10-048-197-2 x BJ069087/rev
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Percent Similarity: 100.000
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Ming,R.A. and Dean,R.A.
A BAC Equencing Framework to Sequence the Rice Genome Unpublished (1998)

Contact: Wing RA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100 Jordan Hall, (Tel: 864 656 7288 Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oryza sativa.
Oryza sativa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: rwing@clemson.edu
Seq primer: GTAAAACGACGGCCAGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clemson University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Clemson University Genomics Institute
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         111
/organism="Oryza sativa"
/strain="Japonica"
/cultivar="Nipponbare"
/db_xref="taxon:4530"
                                                                                                                                                                                                                                                                                                                                                                  /clone="OSJNBb0088N06f"
/clone_lib="CUGI Rice BAC Library (EcoRI)"
                                                                                                                                                                                                                                                                                                                                                    /tissue_type="Leaf"
                                                                                                                                                                                                                                                                                                                                     /lab_host="E. coli DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ocation/Qualifiers
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ORIGIN

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alignment_block:
US-10-048-197-2 x AQ088615
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US-10-048-197-2 x AZ046905
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Ratio: 1.000
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7 ArgLeuThrIleSerAlaLeuLeu 14
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                                                                                                                                                        Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: jwallace@u.washington.edu
Sequence Tagged Connector
Plate: 2208 row: H column: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 409) Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T., Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        409 bp DNA linear GSS 26-AUG-1998 sapiens genomic clone Plate=2208 Col=3 Row=H, DNA sequence. AQ088615
AQ088615.1 GI:3457526
                                                                                                                                                                                                                                                                                                                                                                                         High quality sequence stop: 409.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618.
Fax: (206) 616-3887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Mahairas GG, Wallace JC,
High Throughput Sequencing Center
University of Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
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100.000
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E-Coli DH10B"
                                                                                                                                                                                                                                                                                           /sex-"male"
                                                                                                                                                                                                                                                                                                  /clone="Plate=2208 Col=3 Row=H"
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                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
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TCAGCGCTTCTTACAGCTTTGCTC 114

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11 SerAlaLeuLeuThrAlaLeuLeu 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             High quality sequence stops: 356
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: T7
High quality sequence stop: 356.
Location/Qualifiers
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Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J. Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.
The WashU-Merck EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N39807 410 bp mRNA linear EST 22. yx93b05.rl Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:269265 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (1995)
Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: est@watson.wustl.edu
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/sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="GDB:3878907"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="IMAGE:269265"
                                                from:
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LOCUS AZ132522
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LOCUS BJ072077
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Ratio: 1.000
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                (bases 1 to 427)
Wing, R.A. and Dean, R.A.
A BAC End Sequencing Framework to Sequence the Unpublished (1998)
Contact: Wing RA
                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoldeae; Oryzeae; Oryza.
                                                                                                                                                                             Oryza sativa.
Oryza sativa
                                                                                                                                                                                                                                                                              AZ132522

427 bp DNA linear GSS 02-JUN-20 OSJNBb0070Hllf CUGI Rice BAC Library (ECORI) Oryza sativa genomic Clone OSJNBb0070Hllf, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center For Genetic Resource Information National Institute of Genetics 1111 Yata, Mishima, Shizuoka 411-8540, Japan Tel: 81-559-81-6856 Fax: 81-559-81-6855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BJ072077

411 bp mRNA linear EST 11-DEC-2001
BJ072077 NIBB Mochii normalized Xenopus tailbud library Xenopus
Laevis cDNA clone XL096h02 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 411)
Kitayama, A., Terasaka, C., Mochii, M., Ueno, N.,
Clemson University Genomics Institute
                                                                                                                                                                                                                                          AZ132522.1 GI:8211144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             African clawed frog.
Xenopus laevis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BJ072077.1 GI:17502266
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Xenopus laevis"
/db_xref="taxon:8355"
/clone="XL096h02"
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85 c 107 g
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                                                            Rice Genome
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LOCUS BE685620
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Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Verte
Eukaryota; Metazoa; Chordata; Craniata; Verte
Mammalia; Eutheria; Rodentia; Sciurognathi; M
1 (bases 1 to 430)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
                                                                                                                                                                                                                                                             430 bp
uu56d10.x1 Soares_thymus_2NbMT M
IMAGE:3375955 3', mRNA sequence.
BE685620
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: 864 656 7288 Fax: 864 656 4293
                                                                                                                                                                                                                               BE685620.1 GI:10073296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clemson University
                                                                                                                                                            house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          High quality sequence start: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: rwing@clemson.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100 Jordan Hall,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone-lib="COURDING FILE BAC Library (ECORI)"
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/lab
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BAC/EST Resource Center
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /strain-"Japonica"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Clemson,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22
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6
                                                                  Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                            Mus
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                                                                                                                                                                                                                                                                                                                            musculus
                                                                                                                                                                                                                                                                                                                                                             mRNA
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                                                                                                                                                                                                                                                                                                                                                          linear
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alignment_scores:
    Quality:
    Ratio:
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US-10-048-197-2 x BE685620/rev
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ORIGIN
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                                                                                                                                                                                  Align seg 1/1 to reverse of: BE685620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURES
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Ratio: 1.000
Percent Similarity: 100.000
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source
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This clone is available royalty-free through LLNL; contact the IMAGE Consortium (infoêtmage.llnl.gov) for further information. MGI:1085559.
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/lab_host="DHIDB"
/lab_host="DHIDB"
/lab_host="Thymus"
/lab_host="DHIDB"
/la
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/strain="C57BL/6J"
/db_xref="taxon:1090"
/clone="ImAGE:3375955"
/clone_lib="Soares_thymus_2NbMT"
/sex="male"
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Gaps: 0
Percent Identity: 100.000
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OM of: US-10-048-197-2 to: N\_Geneseq\_032802:\*

out\_format : pfs

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Search information block:
Ouery: US-10-048-197-2
Ouery length: 111
                                                                                                                                                                                                                                                                                                                                                                                                                    Database: N_Geneseq_032802:*
Database sequences: 1736436
Database length: 858457221
Search time (sec): 277.840000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Command line parameters:
                                                                                                                                                                                                                                                                                                                                     /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:AAF59778
/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:AAF28551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -MODEL-frame+_p2n.model -DEV=xlp
-(q-/cgn2_1/USPTO_spool/US10048197/runat_17092002_135957_23607/app_query.fasta_1.168
-DB=N_Geneseq_032802 -OFMT=fastap -SUFFIX=ol1.rng -GAPOP=4.500
-GAPEXT=0.050 -MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000
-GAPEXT=0.050 -MINMATCH=0.100 -LOOPCL=0.000 -YGAPEXT=60.000
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-THR_MIN=1 -ALIGN=40 -MODE=LOCAL -OUTFMT=FS -NORM-ext
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                                                                                                                                                                                                                                                                                                                                                                                           XGAPOP and YGAPOP must be equal. Assuming YGAPOP-XGAPOP-60.000 XGAPEXT and YGAPEXT must be equal. Assuming YGAPEXT-XGAPEXT-60.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sep 18, 2002 10:24 AM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Results were produced by the GenCore software, version 4.5 Copyright (c) 1993-2000 Compugen Ltd.
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47.88
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107.02
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189.07
202.99
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2.1e+03
2.5e+03
2.5e+03
2.5e+03
4.1e+03
4.9e+03
2.4e+04
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241.23
299.58
384.42
404.42
406.33
712.60
852.67
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124.35
124.35
124.35
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2.5e-100
26.74
47.50
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AC AAF59778;
AC AAATTHALIS CATATHALIS
AC AAF59778;
AC AAF59778;
AC AAF59778;
AC AAATTHALIS
AC AAF59778;
AC AAF59778;
AC AAF59778;
AC AAF59778;
AC AAATTHALIS

                                                                                                                                                                             CC The invention relates to the Moraxella catarrhalis strain ATCC43617
CC BASB122 and BASB124 proteins (AAB60640 and AAB60641, respectively). The BASB122 and to DNA encoding them (AAF59778 and AAF59779, respectively). The CC invention also relates to immunogenic fragments of the BASB122 and CC BASB124 proteins, expression vectors and host cells comprising BASB122 or CC or BASB124 nuccine compositions comprising the BASB122 or BASB122 or CC or DASB124, vaccine compositions comprising the BASB122 or BASB122 or CC compositions comprising a manti-BASB122 or BASB124 therapeutic compositions comprising a mati-BASB122 or BASB124 therapeutic compositions comprising a mati-BASB122 or BASB124 therapeutic compositions of the invention are useful as prophylactic or therapeutic compositions of BASB122 or BASB124 proteins or antibodies. The vaccine compositions of the invention are useful as prophylactic or therapeutic agents against Moraxella catarrhalis infections in mammals, particularly isolated from the human upper respiratory tract, which is responsible for could be seen and interventions and insertions in the dearly people, and sinusitis, consocomial infections and, less frequently, invasive diseases. BASB122 or BASB124 proteins or nucleotides may additionally be used in screening for covel antibacterial compounds, and in the diagnosis and staging of infections. The present sequence are presented and some of contrains the warrant and in the diagnosis and staging of infections. The present sequence are presented to the protein of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_name:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New BASB122 and BASB124 polypeptides and polynucleotides from Moraxella catarrhalis strain ATCC 43617, useful as therapeutic agents or vaccines against bacterial infections, e.g. otitis media or pneumonia \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAF59778 standard; DNA; 336
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hearing loss; deafness; pneumonia; sinusitis; nosoc
invasive disease; antibacterial; auditory; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Moraxella catarrhalis strain ATCC43617 BASB122 DNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
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DB; AAB60640.
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                                                                                                          The present sequence represents DNA encoding strain ATCC43617 BASB122 protein.
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99GB-0018036
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sinusitis; nosocomial infection;
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106 A;

65 Ç 61 <u>ن</u>

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seq_documentation_block:
ID AAF28551 standard; DN
XX
AC AAF28551;
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AC AAF28551;
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DT 04-APR-2001 (first e
XX
Genomic library; bact
XX
DF WO200078968-A2.
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PD 28-DEC-2000.
XX
PP 16-JUN-1999; 99US-(
XX
PR 18-JUN-1999; 99US-(
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PA (INCY-) INCYTE GENOM.
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US-10-048-197-2 x AAF59778
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Genomic library for identifying diagnostic and therapeutic compositions, and for identifying virulence factors, regule elements and drug targets, comprises Moraxella catarrhalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genomic library; bacteria; human upper airway; otitis media; sinusitis; bronchopulmonary; endocarditis; meningitis; ss.
                                                                                                                                                                                                                                (INCY-) INCYTE GENOMICS INC.
                                                                                                                                                                                                                                                                                                                                        16-JUN-2000; 2000WO-US16649.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Moraxella catarrhalis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genomic fragment #38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                lulleLeuSerLeuIleIleSerPheLeuTrpValLysProTyrArgPro 100
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Ratio:
                                                                                                                                                                          Patterson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                 99US-0140121.
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  catarrhalis nucl
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ID AAH65480 standard;
                                                                                                                                                                                                                                             seq_name: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:AAH65480
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US-10-048-197-2 x AAF28551
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Ratio: 1.000
Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               75267 ATGTTAAATCATCATATTCGCCTGACTATTCCGCTTTACTGACGGCACT
                                                    Coryneform bacterium; amino acid synthesis; vitamin; saccharide; organic acid synthesis; ds.
                                                                                                   C glutamicum coding sequence fragment SEQ ID NO:
                          Corynebacterium glutamicum
                                                                                                                                        26-SEP-2001
                                                                                                                                                                         AAH65480;
                                                                                                                                                                                                                                                                                                 101 LysAsnLeuSerPheTyrLeuThrAlaLysAla 111
                                                                                                                                                                                                    AAH65480 standard;
                                                                                                                                                                                                                                                                                                                                                          84 luIleLeuSerLeuIleIleSerPheLeuTrpValLysProTyrArgPro 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to a Moraxella catarrhalis genomic library comprising of a combination of 41 nucleic acid molecules (see AAF28514-AAF28554). The library has a number of uses described in the specification e.g. is useful for aidentifying diagnostic and therapeutic compositions. M. Catarrhalis (Branhamella catarrhalis) is a large aerobic, gram-negative diplococcus, normally found among the bacterial flora of human upper airways. M. catarrhalis is known to cause acute, localised infections such as otitis media, sinusitis and bronchopulmonary infection and life-threatening, systemic diseases including endocarditis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51
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                                                                                                                                                                                                                                                                                AAGAACTTGTCATTTTATTTGACAGCAAAGGCA 75599
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                                                                                                                                    (first entry)
                                                                                                                                                                                                    DNA;
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EP1108790-A2

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alignment_scores: 8.00
Quality: 8.00
Ratio: 1.000
Percent Similarity: 100.000
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US-10-048-197-2 x AAH65480
                                                                                                                                                                                                                                                    seq_name: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:AAI89885
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                                                                                                                                                                                                          _documentation_block:
AAI89885 standard; cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a nucleic acid described in the exemplification of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the European Patent Office.
                                         Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopolesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-376931/40.
P-PSDB; AAG90261.
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Tateishi N,
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07-APR-2000;
                                                                                                                     Human
                                                                                                                                                06-NOV-2001
                                                                                                                                                                               AAI89885;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 261
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                                                                                                                                                                                                                                                                                   polynucleotide
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2000JP-0159162.
2000JP-0280988.
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Senoh A,
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                                                                                                                                                (first entry)
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                                                                                                                    SEQ ID
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Gaps:
Percent Identity:
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seq_documentation_block:
ID AAX13630 standard; DN
XX
AC AAX13630;
XX
DT 19-MAR-1999 (first e
XX
DE Enterococcus faecalis
XX
W Enterococcus faecalis
XX
Vaccine; attenuation;
XX
PN W09850555-A2.
XX
PD 12-NOV-1998.
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US-10-048-197-2 x AAI89885
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AA000010-AA013910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and
                                                                                                                                                                                                                                                                                                                                       348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukaemia, inflammation and immun
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18-MAY-2000; 2000US-0577409
                                                                                                                     Enterococcus faecalis; contig;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 479 BP; 103 A; 97 C; 102 G; 176 T;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Note: The sequence data for this patent did not form specification, but was obtained in electronic format
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID NO 9945; 1399pp + Sequence Listing; English
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                                                                                                                                                                                                                                                                                                                                       CTAAGCTTAATCATTTCTTTCTT
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                                                                                                    attenuation;
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                                                                                                                                                  faecalis genome
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100.000
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                                                                                                    computer
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                                                                                                        readable medium;
                                                                                                                     detection; Enterococcal infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Identity:
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seq_documentation_block:
ID ABK16762 standard; cC
XX
AC ABK16762;
XX
DT 14-MAR-2002 (first e
XX
DT 14-MAR-2002 (first e
XX
DT 14-MAR-2002 (first e
XX
CN Human cDNA encoding G
XX
KW Human; ss; G protein-
KW rheumatoid arthritis;
KW CN disorder; migrair
KW rheumatoid arthritis;
KW CNS disorder; migrair
KW manic depression; sch
KW dyskinesia; Huntingtc
KW degenerative disorder
KW viral infection; HIV
KW human immunodeficienc
KW cobesity; anorexia; hy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_block:
US-10-048-197-2 x AAX13630
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Percent Similarity:
             rheumatoid arthritis; autoimmune disorder; movement disorders; CNS disorder; migraine; neurological disorder; anxlety; manic depression; schizophrenia; epilepsy; severe mental retardation; dyskinesia; Huntington's disease; Tourette's syndrome; degenerative disorder; parkinson's disease; Alzhelmer's disease; viral infection; HIV infection; cardiovascular disorder; human immunodeficiency virus; metabolic disorder; type II diabetes;
                                                                                                                                              Human; ss; G protein-coupled receptor; nGPCR-x; thyroid disorder; thyreotoxicosis; renal failure; inflammatory condition; Crohn's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A computer readable medium has been developed which has recorded on it 982 nucleotide sequences isolated from the Enterococcus faecalis genome. Primary nucleotide sequences these nucleotide sequences which are primary nucleotide sequences, also known as contigs. The computer-based commercial importance. The products can be used to detect the presence diagnosing Enterococcus faecalis in samples. They can also be used for progression of disease, and for identifying agents which can be used to modulate the growth or pathogenicity of Enterococcus faecalis, or another related organism, in vivo or in vitro. In particular the polypeptides encoded by the Enterococcus faecalis nucleotide sequences can be used in vaccines to prevent or attenuate an Enterococcal
                                                                                                                                                                                                             Human cDNA encoding G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-NOV-1997;
06-MAY-1997;
16-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 1931-1932; 2084pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                           65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated Enterococcus faecalis polynucleotides and polypeptides - used to develop products for the detection of Enterococcus and for use in vaccines for prevention or attenuation of Enterococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               04-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                             ArgLeuThrIleSerAlaLeuLeu 14
                                                                                                                                                                                                                                                                                                                                                                                                                     CGTTTAACAATTTCAGCACTTTTA 88
                                                                                                                                                                                                                                                                                                                                                                         /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:ABK16762
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100.000
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97US-0044031.
97US-0046655.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        140
   hypotension; hypertension;
                                                                                                                                                                                                                                                                                                                            cDNA; 562 BP
                                                                                                                                                                                                                                                   entry)
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                                                                                                                                                                                                         protein-coupled receptor nGPCR-Seq2664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              from: 1
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6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.000
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   myocardial
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cc autolumune disorders, movement disorders, CNS disorders (e.g. pain concluding migraine, stroke, psychotic and neurological disorders including migraine, stroke, psychotic and neurological disorders concluding anxiety, mental disorders, manic depression, generalised concluding anxiety, mental disorders, manic depression, generalised concluding anxiety disorders, post-traumatic-stress disorders, schizophrenia, concluding anxiety disorders described as Huntington's disease or Tourette's concluding attains, concluding att
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         polynucleotides, termed ndpCR-x, and the ndpCR-x proteins. The ndpCPCP-x proteins, polynucleotides, anti-ndpCR-x antibodies, and modulators ndpCR-x are useful for the diagnosis and treatment of diseases or conditions such as thyroid disorders (thyreotoxicosis), renal fall inflammatory conditions (Crohn's disease), disease related to cell differentiation and homeostasis, rheumatold arrhritts,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-MAY-2000;
22-MAY-2000;
02-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel G-protein-coupled receptor polypeptides and polynucleotides useful for diagnosis, prevention and treatment of viral infections, cancer, metabolic, cardiovascular diseases and neurological disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (PHAA ) PHARMACIA & UPJOHN CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       atherosclerosis; cancer; hyperproliferative disorder; psorlasis; hormonal disorder; polycystic ovarian syndrome; sexual dysfunction; respiratory allment; asthma; traumatic brain injury; angina; glucose uptake disorder; metabolic disorder; angiogenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22-MAY-2001; 2001WO-US16419
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                                                                                         metabolism, rac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2002-106173/14
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562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Page 71; 138pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; 2000US-206138P.
; 2000US-206139P.
; 2000US-208976P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      relates to novel G-protein-coupled receptor es, termed nGPCR-x, and the nGPCR-x proteins
                                                                               fatty acid uptake, abnormal angiogenesis, the present sequence is a cDNA encoding a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        wound healing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       proteins. The nGPCR-x es, and modulators of
                                                                                                                              vasculogenesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        failure,
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alignment\_block: US-10-048-197-2 x ABK16762/rev

Align seg 1/1

to reverse of: ABK16762

from: Н

to:

alignment\_scores:
 Quality:

Sequence

BP;

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₽, 118

C; 140 G; 128 T; 0

other;

Percent Similarity:

Ratio:

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Percent

Identity:

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alignment_scores:
Quality:
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ID AAH05525 standard;
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                                                                                                                                                     cc complementary strand of a polynucleotide which complementary to the complementary strand of a polynucleotide which comprises a 5'-end cc sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence complementary to a cc polynucleotide comprises a 1'-end sequence, where the cc the 5'-end sequence/3'-end sequence is selected from those defined in cc the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proceins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and Cc AAH3633 to AAH18742 represent human cDNAs sequences; AAB92446 to CC AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29-JUL-1999;
27-AUG-1999;
11-JAN-2000;
02-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide comprises one of the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of a polynucleotide comprises at least 15 nucleotides; or (b) a combination
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Primer sets for synthesizing polynucleotides, particularly full-length cDNAs defined in the specification, and for the and/or diagnosis of the abnormality of the proteins encoded full-length cDNAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ota T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAH05525;
                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ishii S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-JUN-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID 2360; . 2537pp + CD ROM;
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2000JP-0183767.
2000JP-0241899.
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                                                                                                            184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nishikawa T,
T, Wakamatsu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hayashi K,
A, Nagai K,
                                                                                                         <u>.</u>
                                                                                                            149
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Otsuki
                                                                                                            other;
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reverse of: AAQ62008

from:

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alignment_block:
US-10-048-197-2 x AAH05525
alignment_block:
US-10-048-197-2 x AAQ62008/rev
                                                                                               alignment_scores
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ID AAQ62008 standard;
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                                                                                                                                                                                                            The yeast sec1 suppressor gene SSO2 was isolated as a supreesor of the temperature sensitive defect of the sec 1-1 mutant. When overexpressed in eukaryotic cells the gene renders the cells capable of producing increased amts. of secreted proteins, e.g. antibodies or hydrolytic enzymes. The gene may be used for more efficient biomass produc. from raw material or efficient hydrolysis of a raw
                                                                                                                                                                                              materia.
                                                                                                                                                                                                                                                                                                                            Claim 3; Page 32; 51pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1994-135588/16.
P-PSDB; AAR51274.
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                                                                                                                                                Sequence 885
                                                                                                                                                                                                                                                                                                                                                             New secl suppressor gene - used for increasing prodn of secreted foreign or endogenous proteins by eukaryotic cells
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27-APR-2000; 2000US-0560875.

20-JUN-2000; 2000US-0598075.

19-JUL-2000; 2000US-0620325.

01-SEP-2000; 2000US-063936.

15-SEP-2000; 2000US-0634936.

20-OCT-2000; 2000US-063325.

20-OCT-2000; 2000US-0728422.
                                                                                                                                                                                                                                                                                        The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activiny inhibin activity and may be useful in the diagnosis and/or inflammation.
                                                                                                                                                               Sequence
                                                                                                                                                                                                       Note: Records for SEO ID NO 2110 (AAK52581), (AAM80020) are omitted as the relevant pages were missing at the time of publication.
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AAK53351 standard; cDNA; 911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 5035; 6221pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tang YT, Liu C, Drmanac RT, Asundi V, Zhao QA, Wang D, Wang J, Zhang J, Ren Xue AJ, Yang Y, Wejhrman T, Goodrich R;
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P-PSDB; AAM80218.
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Arabidopsis thaliana DNA fragme

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PP 06-SEP-2000; 2000EP-0301439.

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PP 25-FEB-1999; 99US-0125148.

PR 25-MAR-1999; 99US-0125788.

PR 05-MAR-1999; 99US-0126785.

PR 05-MAR-1999; 99US-0126785.

PR 05-MAR-1999; 99US-0126785.

PR 05-MAR-1999; 99US-0126785.

PR 06-APR-1999; 99US-0128714.

PR 10-APR-1999; 99US-0130419.

PR 11-APR-1999; 99US-0130449.

PR 12-APR-1999; 99US-013048.

PR 13-APR-1999; 99US-013048.

PR 14-MAY-1999; 99US-0132486.

PR 06-MAY-1999; 99US-0132486.

PR 06-MAY-1999; 99US-0134218.

PR 14-MAY-1999; 99US-0134218.

PR 14-MAY-1999; 99US-0134266.

PR 14-MAY-1999; 99US-0134266.

PR 14-MAY-1999; 99US-013426.

PR 25-MAY-1999; 99US-013426.

PR 25-MAY-1999; 99US-013426.

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PR 26-MAY-1999; 99US-013426.

PR 27-MAY-1999; 99US-013426.

PR 28-MAY-1999; 99US-013426.

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DNA encoding novel h
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NAME FOR LONG Supplement; medi
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Human; chromosome mag
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Homo sapiens.

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PR

31-MAR-2000; 2000US-1
PR

31-MAR-2000; 2000US-1
PR

31-MAR-2000; 2000US-1
PR

31-MAR-2001; 2001WO-1
XX

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Drmanac RT, Liu C,
XX

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Drmanac RT,
Allex

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Drmanac RT,
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Drmanac RT,
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                                                                                              diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
                                                                  at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                              polymerbide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, cane manning identifications.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to isolated polynucleotide (I) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID No 17692; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                polypeptide (II) sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-MAR-2001; 2001WO-US08631.
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2000US-0649167.
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medical imaging; diagnostic; genetic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cDNA; 1347 BP
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274 A; 331 C;

346 G;

396 T;

0 other

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seq_name: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:AAH15929
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US-10-048-197-2 x AAS81888
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of an oligonuclectide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the oligonucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .29-JUL-1999;
27-AUG-1999;
11-JAN-2000;
02-MAY-2000;
09-JUN-2000;
                                                                                                                                                                                                                                    The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of
                                                                                                                                                                                                          the 5602 nucleotide sequences defined in the specification oligonucleotide comprises at least 15 nucleotides; or (b)
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                                                                                                                                                                                                                               the 5602
                                                                                                                                                                                                                                                                                                                                Claim 8; SEQ
                                                                                                                                                                                                                                                                                                                                                              Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (HELI-) HELIX RES INST.
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; 2000JP-0183767.
; 2000JP-0241899.
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99JP-0300253,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             detection; diagnosis; antisense therapy; gene therapy;
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A, Nagai K,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Otsuki
                                                                                                                                                                                                                                                                                                                                                                        for the detection encoded by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yamamoto
                                                                                                                                                                                                        a combination
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AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAB92893 represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification of the present invention.

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seq_documentation_block:
ID AAK52367 standard; cl
XX
AC AAK52367;
XX
Df 06-NOV-2001 (first e
XX
DT 06-NOV-2001 (first e
XX
DT 06-NOV-2001 (first e
XX
DT 06-NOV-2001; peptide there
KW Human; cytokine; cell
KW vaccine; peptide there
KW tissue growth factor;
KW nervous system disord
XX
Homo sapiens.
XX
VO200157190-A2.
XX
VO3-FEB-2001; 2001W0-L
XX
O3-FEB-2000; 2000US-L
PR 03-FEB-2000; 2000US-L
PR 19-JUL-2000; 2000US-L
XX
PR 19-PSDB; AAM79234.
XX
Nucleic acids encodir
PT useful in diagnosis e
XX
Claim 1; Page 3005-30
CC The invention relates
CC cytokine, cell prolifices
CC cytokine, cell prolifices
CC cytokine, cell prolifices
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US-10-048-197-2 x AAH15929
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The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM73323-AAM80302) that exhibit activity elatif cytokine, cell proliferation or each differentiation or which may inc production of other cytokines in other cell populations. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                             05-FEB-2001; 2001WO-US04098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human polynucleotide SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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Similarity:
                                                                                                                                                            2001-476283/51.
DB; AAM79234.
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                                                                                                          acids encoding polypeptides with in diagnosis and gene therapy -
                                                                                                                                                                                                     Liu C, Drmanac RT, Asundi V,
Wang D, Wang J, Zhang J, Ren
Yang Y, Wejhrman T, Goodrich I
                                                                                                                                                                                                                                                                                                  2000US-0496914
2000US-0560875
2000US-0598075
2000US-0620325
2000US-062325
2000US-063935
2000US-0693325
2000US-0728422
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                                                                           6221pp;
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F, C
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The present invention provides plasmids isolated from Corynebothermoaminogenes encoding a rep protein. These are useful for Coryneform bacteria, which are capable of growing at elevated temperatures and of producing substances such as L-amino acidi present sequence is the coding sequence of the Coryneform bacterial such

New plasmids derived from Corynebacterium thermoaminogenes, improving coryneform bacteria, which can grow at elevated to and for producing useful substances (e.g. L-amino acids)

temperatures,

useful for

Example 2; Page 21-24;

32pp;

English.

Corynebacterium

for improving

bacterial

ds. The

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alignment_scores:
    Quality:
    Ratio:
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                                                                                                                                                                                                                                                                                                                                                                                                                    _documentation_block:
AAF24443 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoisesis regulating activity, tissue growth factor activity, immunomodulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or
                                                                                                                                                    WPI;
                                                                                                                                                                                                                                                                                                        Corynebacterium thermoaminogenes
                                                                                                                                                                                                                                                                                                                                                         Corynebacterium thermoaminogenes plasmid
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                                                                                                                                                                                                                                                                                                                                                                                                 AAF24443;
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                                                                                                                                                                                                                                           11-AUG-2000;
                                                                                                                                                                                                                                                                                     EP1076094-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation.
                                                                                                                                                                       Sugimoto
                                                                                                                                                                                 Matsuzaki Y,
                                                                                                                                                                                                                                                                                                                                     Plasmid;
                                                                                                                                         P-PSDB;
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                                                                                                                                                                                                                        12-AUG-1999;
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                                                                                                                                                                                 Kimura
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                                                                                                                                                                                                                                                                                                                                     bacterium;
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                                                                                                                                                                                 Kurahashi O,
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                                                                                                                                                                                                                                                                                                                                      L-amino acid; thermostable;
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seq_name: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:ABA16230
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           31-JAN-2000

04-FEB-2000

24-FEB-2000

02-MAR-2000

16-MAR-2000

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19-MAY-2000

07-JUN-2000

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ABA16230 standard; DNA; 4604
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2000US-0229509
2000US-0229513
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alignment_scores
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Quality: 8.00
Ratio: 1.000
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08-NOV-2000;
17-NOV-2000;
                                                                                                                                                      Note: The sequence data for this patent did not form printed specification, but was obtained in electronic from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acids encoding useful for preventing, cancers and metastases
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2000US-0229287 2000US-0229344 2000US-0229344 2000US-0229345 2000US-0229509 2000US-0229513 2000US-0230437 2000US-0230437 2000US-0231242 2000US-0231242 2000US-0231243 2000US-0231243 2000US-0231243 2000US-0231243

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Quality:
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Align seg 1/1 to: ABA16231
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17-NOV-2000;
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08-DEC-2000;
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17-NOV-2000;
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    2000US-0179065.
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ID NO 10430

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US-10-048-197-2 x ABA16232
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Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acids encoding 3224 human nervous system antigen polypeptides useful for preventing, diagnosing and/or treating nervous system cancers and metastases -
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                                                               CTCCTGGTCACAGGCTGCGTTTCT 611
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pharmaceutical; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                         (first entry)
system related polynucleotide SEQ ID NO 11286
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100.000
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                                                                                                                                                                                                                                                                                          DNA;
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Gaps:
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| Human: notoropic; neuroprotective; cytostatic; dermatological; viruciammunouppessive; antilnilammator; antil |
| logical; virucide; terial; vulnerary; liammatory; antifungal; ar disorder; arapy; vaccine; ds.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |
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| טיטיטיטיטיטיטיטיטיטיטיטיטיטיטיטיטיטיטי                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
| 14 - SEP - 2000   25 - SEP - 2000   25 - SEP - 2000   27 - SEP - 2000   29 - SEP - 2000   20 - OCT - 2 |
| 2000US-023401. 2000US-0233063. 2000US-0233063. 2000US-023497. 2000US-023497. 2000US-023499. 2000US-0235844. 2000US-0235844. 2000US-0235844. 2000US-0235844. 2000US-0236367. 2000US-0236367. 2000US-0236369. 2000US-0236369. 2000US-0236369. 2000US-0236369. 2000US-0236369. 2000US-0236369. 2000US-0236369. 2000US-0246370. 2000US-0249708. 2000US-0249708. 2000US-0249708. 2000US-0246610. 2000US-0246611. 2000US-0246611. 2000US-0246611. 2000US-0246611. 2000US-0246611. 2000US-0246611. 2000US-0246611. 2000US-0246611. 2000US-0246611. 2000US-0249211. 2000US-0249213. 20 |

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seq_documentation_block: ID ABA19362 standard; DNA; 10126
                                                                                                                                                                                                                                                               seq_name: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:ABA19362
                                                                                                                                                                                                                                                                                                                                                                                                     alignment_block:
US-10-048-197-2 x ABA18955
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                                                                                                                                                                                                                                                                                                                                                                     Align seg 1/1 to: ABA18955
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Quality: 8.00
Ratio: 1.000
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to novel genes (ABA11004-ABA21534) and proteins CC (ABB14678-ABB18001) useful for preventing, treating or ameliorating CC medical conditions e.g. by protein or gene therapy. The genes are CC isolated from a range of human tissues disclosed in the specification. CC The nucleic acids, proteins, antibodies and (ant)ayonists are useful CC in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast CC marrow, breast, gastrointestinal tract, liver, lung, or urogenital; CC marrow, breast, gastrointestinal tract, liver, lung, or urogenital; CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative CC (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and CC epilepsy; and (f) infectious diseases such as wiral, bacterial, fungal CC note: The seminance data for this patent did not form.
                                                                                                                                                                                                                                                                                                          8429
             antirheumatic; hepatotropic; cerebroprotective; antiin; antiallergic; antidiabetic; antiulcer; anticonvulsant;
                        Human; nootropic; neuroprotective; cytostatic; dermatological; virucide; immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary; antiparkinsonian; antisickling; antianaemic; antiarthritic; cancer; antitheumatic; hepatotropic; cerebroprotective; antiinflammatory;
        antiparasitic;
                                                                                                                         Human
                                                                                                                                                     23-JAN-2002 (first entry)
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08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
11-DEC-2000;
05-JAN-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                   AAGCAAGAAATATCAAGTAGGTTT 8452
                                                                                                                                                                                                                                                                                                                      LysGlnGluIleSerSerArgPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The sequence data for this patent did not form potted specification, but was obtained in electronic wife at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                               nervous system related polynucleotide SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2001-541565/60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     acids encoding 3224 human nervous system antigen polypeptides, for preventing, diagnosing and/or treating nervous system and metastases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Barash
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 11286; 1701pp + Sequence Listing; English.
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; 2000US-0251868.
; 2000US-0251869.
; 2000US-0251989.
; 2000US-0251990.
; 2000US-0254097.
; 2001US-0259678.
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     immune
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   disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Length: 8
Gaps: 0
Identity: 100.000
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   cardiovascular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2749
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                                                                                                                  NO 11693.
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c format directly
                 antifungal;
disorder,
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WW meurological disease; infection; nephrotropic; gene therapy; vaccine; New Mozool5963-A2.

W Mozool5963-A2.

W Mozool5963-A2.

W Mozool5963-A2.

W Mozool5963-A2.

W Mozool5963-A2.

W Mozool2001.

W Mozool5963-A2.

W Mozool6963-A2.

W Mozool6963
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27-SEP-2000;
27-SEP-2000;
27-SEP-2000;
29-SEP-2000;
29-SEP-2000;
29-SEP-2000;
29-SEP-2000;
29-SEP-2000;
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02-OCT-2000;
02-OCT-2000;
02-OCT-2000;
                         2000US-0234998.
2000US-0235836.
2000US-0235836.
2000US-0235836.
2000US-0236369.
2000US-0236369.
2000US-0236369.
2000US-0237038.
2000US-0237039.
2000US-0237039.
2000US-0237039.
2000US-0237039.
2000US-02341809.
2000US-0241785.
2000US-0241786.
2000US-0241787.
2000US-0246475.
2000US-0246477.
2000US-0246610.
2000US-0246611.
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2000US-024661.
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2000US-024921.
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Quality:
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ID AAL36875 standard; DNA; 12167
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US-10-048-197-2 x ABA19362/rev
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ratio: 1.000 Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Align seg 1/1 to reverse of: ABA19362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant; antibacterial; antiinflammatory; antiparasitic; cardiant; gene therapy; cancer; lmmune disorder; cardiovascular disorder; neurological disease; infection; human; secreted protein; musculoskeletal system; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroidittis, diabetes multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological disease e.g. cerebral anoxia and gollepsy; and (f) infectious diseases such as viral, bacterial, fungal and parasitte infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to novel genes (ABA11004-ABA21534) and proteins (ABB14678-ABB18001) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification.
                                                                                                                       Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cancers and
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                         02-AUG-2001
                                                                         WO200155367-A1
                                                                                                                                                                                                                                                                                          Cytostatic; immunosuppressive; nootropic; neuroprotective;
                                                                                                                                                                                                                                                                                                                                       Human musculoskeletal system related polynucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                       sapiens.
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31-JAN-2000

04-FEB-2000

24-FEB-2000

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11-MAR-2000

11-MAR-2000

11-MAR-2000

11-MAR-2000

11-MAR-2000

11-JUL-2000

11-JUL-2000

11-JUL-2000

11-JUL-2000

14-AUG-2000

14-SEP-2000

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               2000US-0179065
2000US-0180628
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2000US-01806350
2000US-0198123
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17-NOV
Isolated polypeptide for treating, preventing {	t and/} or {	t prognosing}
                                                                                                               (HUMA-)
                                           2001-451937/48
                                                                                                                 HUMAN
                                                                                                                                                 2000US-0236370.
2000US-0237039.
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2000US-0259499.
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2000US-0259499.
2000US-0259186.
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alignment_block:
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Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to novel genes (AAL34669-AAL37666) and proteins (C (ABB03087-ABB04109) associated with the musculoskeletal system useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gother cancers of the adrenal gland, bone, bone marrow, breast, alternative e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular discorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ratio:
Percent Similarity:
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31-JAN-2000;
04-FEB-2000;
24-FEB-2000;
                                                                                                                                                                                                                       immunosuppressive; antiinflammatory; anti-HTV; antibacterial; vulne; antiparkinsonian; antistickling; antianaemic; antiarthrittc; cancer; antirheumatic; hepatotropic; cerebroprotective; antiinflammatory; antiallergic; antidiabetic; antiulcer; anticonvulsant; antifungal; antiparasittc; cardiant; immune disorder; cardiovascular disorder; neurological disease; infection; nephrotropic; gene therapv: vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     parasitic infections.

Note: The sequence data for this patent did not form parameters appeared in electronic parameters are from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                         Human; nootropic; neuroprotective; cytostatic; dermatological; virucide;
immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 12167 BP; 3252 A; 2986 C; 2599 G; 3330 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  disorders related to the musculoskeletal system including musculoskeletal cancers and also for testing and detection
                                                                            17-JAN-2001;
                                                                                                                                                      WO200159063-A2
                                                                                                                                                                                                                                                                                                                                                                                                                       23-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABA19852;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABA19852 standard;
                                                                                                                 16-AUG-2001
                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                  Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 88 LeuIleIleSerPheLeuTrpVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTGATAATTTCTTTCCTTTGGGTA 10894
                                                                                                                                                                                                                                                                                                                                                                                  nervous system related polynucleotide SEQ ID NO 12183.
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2000US-0184664.
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                                                                            2001WO-US01334
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Gaps:
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   14-SEP-2000;
21-SEP-2000;
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25-SEP-2000;
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16-MAR-2000;

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18-APR-2000;

19-MAY-2000;

07-JUN-2000;

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05-DEC-2000;
06-DEC-2000;
08-DEC-2000;
08-DEC-2000;
   Disclosure; SEQ ID NO 12183; 1701pp + Sequence Listing; English
                                          Nucleic acids encoding useful for preventing,
                                                                                                                                                                                                                                                                                                                                                                              17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
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17-NOV-2000;
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                                                                            2001-541565/60.
                                                                                                                        HUMAN
                                                                                                  Barash
                                 metastases
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2000US-0251160.
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2000US-0246474.
2000US-0246475.
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2000US-0239935
                                                                                                 SC,
                                                                                                                      SCI INC.
                                  diagnosing
                                                                                               Ruben
                                                                                               SM;
                                        nervous
and/or t
                                    s system antigen polypeptides, treating nervous system
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31-JAN-2000; 04-FEB-2000; 24-FEB-2000; 02-MAR-2000; 16-MAR-2000; 17-MAR-2000;

2000US-0179065. 2000US-0180628. 2000US-0184664. 2000US-0186350. 2000US-0189874. 2000US-0190076.

17-JAN-2001; 02-AUG-2001. WO200155321-A2

2001WO-US01340.

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seq_name: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:AAS36105
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US-10-048-197-2 x ABA19852
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Ratio: 1.000
Percent Similarity: 100.000
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AAS36105 standard;
                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                 anti-infertility.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and parasitic infections.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to novel genes (ABAll004-ABA21534) and proteins (ABB14678-ABB18001) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-DEC-2001 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cardiovascular system antigen genomic DNA SEQ ID No 1605.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                standard; DNA; 32195
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Gaps: 0
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20-OCT-2000

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Sequences AAS35741-AAS36942 represent genomic DNA molecules, which the cardiovascular system antigen polypeptides of the invention. Cardiovascular system antigens and their associated polynucleotides
                                                            Claim
                                                                                         New cardiovascular system related polynucleotides useful for diagnosing, treating and/or preventing cardiovascular system -
                                                                                                                                                                                       Rosen
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                                                            English.
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2000US-0225377
2000US-02257733

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alignment_scores: 8.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cc useful in the diagnosis, treatment and prevention of various types of cdisorders in e.g. humans, mice, rabbits, goats, horses, cats, dogs, cc chickens or sheep. A pathological condition can be determined by cd detecting the presence or absence of a mutation in a cardiovascular condition can be determined by cc diseases such as rheumatoid arthritis, hyperproliferative disorders such as neoplasms of the breast or liver, cardiovascular disorders such as cc cardiac arrest, cerebrovascular disorders such as cerebral ischaemia, cnervous system disorders such as Alzheimer's disease, infections caused by bacteria, viruses and fungi, ocular disorders such as corneal confection, endocrine disorders such as premature labour and infertility, gastrointestinal disorders such as crohn's disease, renal disorders such as glomerulonephritis and respiratory disorders such as asthum and confection, the polypeptides can also be used to aid wound healing, to prevent skin aging due to sunburn, to maintain organs before transplantation, to regenerate tissues and in chemotaxis.

Note: The sequence data for this patent did not form part of the printed constants in the form hand in the format directly from WIPO
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04-FEB-2000;
24-FEB-2000;
02-MAR-2000;
16-MAR-2000;
17-MAR-2000;
                                                                                                                                                                                                                                                                                                     Human; secreted extracellular matrix protein; ds; immunomodulatory; Anti-HIV; antianemic; antirheumatic; antisclerotic; cardiant; vascular; cerebroprotective; thrombolytic; antimicrobial; ophthalmic; cytostatic; antialzheimers; immune/autoimmune disease; HIV infection; anaemia; human immunodeficiency virus; rheumatoid arthritis; multiple sclerosis; cancers; hyperproliferative disorder; breast neoplasm; melanoma; Sezary syndrome; Gaucher's disease; neurological diseases; Sezary syndrome; Gaucher's disease; neurological diseases; Alzheimer's disease; Parkinson's disease; cardiovascular disorder; cardiac arrest; tachycardia; angina; infection; corneal infections; cardiac arrest; tachycardia; angina; infection; corneal infections;
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AAS31532 standard; DNA; 32195
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                                                                                                                                                                                                                                                                                  Homo sapiens.
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08-NOV-2000;
08-NOV-2000;
   The invention relates to isolated nucleic acid molecules encoding novel human secreted extracellular matrix proteins (SPs). The polynucleotides and proteins are used to prevent, treat a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. For example, disorders associated with decreased
                                                                                                                                          Nucleic acid molecules encoding human secreted extracellular matrix proteins, used in preventing, treating or ameliorating a disorder, allzheimer's and Parkinson's diseases and cancers -
                                                                                                             Claim
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include
support
                                  antagonists may also be used to down regulate expression and activity of sp and as diagnostic agents for detecting the presence of SPs in samples. The disorders include for example: immune/autoimmune diseases (e.g. HIV (human immunodefictency virus) infections, anaemia, rheumatoid arthritis and multiple sclerosis), cancers and hyperproliferative disorders (e.g. melanomas, neoplasms of the breast or liver, Sezary syndrome and Gaucher's disease), neurological diseases (e.g. Alzheimer's disease, parkinson's disease) cardio-/cerebrovascular disorders (e.g. cardiac arrest, tachycardia and angina), infections caused by bacteria, viruses and fungi and ocular disorders (e.g. corneal infections). Other uses include wound healing, maintenance of organs before transplantation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                expression of SPs. The SP polynucleotide or a vector expressing them may be administered to treat diseases by gene therapy. Antisense molecules may be administered to down regulate expression of SPs by binding with the cells own genes and preventing their expression. The polynucleotides may also be used as DNA probes in diagnostic assays. The SPs may also be used as antigens to produce antibodies and to identify modulators (agonists and antagonists) of the SPs. The anti-(SP) antibodies and
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         cell
    culture
    of primary tissues,
    modulation
         of.
              for
    example
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Human; secreted extracellular matrix protein; ds; immunomodulatory; anti-HIV; antianemic; anti-Heumatic; antisclerotic; cardiant; vascular; cerebroprotective; thrombolytic; antimicrobial; ophthalmic; cytostatic; antialzheimers; immune/autoimmune disease; HIV infection; anaemia; human immunodeficiency virus; rheumatoid arthritis; multiple sclerosis; cancers; hyperproliferative disorder; breast neoplasm; melanoma; Sezary syndrome; Gaucher's disease; neurological diseases; Parkinson's disease; cardiovascular disorder; Alzheimer's disease; Parkinson's disease; cardiovascular disorder; arrest; tachycardia; angina; in: ealing; immunogen; gene therapy; infection; corneal antisense; infections; additive.

2001WO-US01348

2000US-0179065. 2000US-0180628. 2000US-0184664. 2000US-0186350. 2000US-0189874. 2000US-0198123. 2000US-0198123. 2000US-0205515. 2000US-0209467.

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The invention relates to isolated nucleic acid molecules encoding novel human secreted extracellular matrix proteins (SPs). The polynucleotides and proteins are used to prevent, treat a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. For example, disorders associated with decreased expression of SPs. The SP polynucleotide or a vector expressing then
                                                                                                                                                            Nucleic acid molecules encoding human secreted extracellular matrix proteins, used in preventing, treating or ameliorating a disorder, earlichemer's and Parkinson's diseases and cancers -
                                                                                                                               Claim
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    The invention relates to an isolated nucleic capable of detecting 1000 or more genes from
                                                                         Claim 1; SEQ ID NO 9338; 21pp + Sequence Listing; English
                                                                                                                         New isolated nucleic acid genes from Drosophila and interactions -
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invention

The present invention relates to a Moraxella catarrhalis genomic library comprising of a combination of 41 nucleic acid molecules (see AAF28514-AAF28554). The library has a number of uses described in the specification e.g. is useful for aldentifying diagnostic and therapeutic compositions. M. catarrhalis (Branhamella catarrhalis) is a large

Claim 1; Page 309-324; 545pp; English

aerobic, gram-negative diplococcus, normally found among the bacterial flora of human upper airways. M. catarrhalis is known to cause acute, localised infections such as otitis media, sinustitis and bronchopulmonary infection and life-threatening, systemic diseases including endocarditis

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MO200078968-A2.
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                                                                                                                                                                                                                                                                                                                                                              Genomic library for identifying diagnostic and therapeutic compositions, and for identifying virulence factors, regulatory elements and drug targets, comprises Moraxella catarrhalis nucleic acids -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genomic library; bacteria; human upper airway; bronchopulmonary; endocarditis; meningitis; ss
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 The present invention relates to the genomic sequence of Pyrococcus abyssi and P. abyssi proteins (see AAB96053-AAB96842). P. abyssi is a hyperthermophilic archaeon, which is isolated from deep-sea hydrothermal vents. The present sequence is a fragment of the genomic sequence of P. abyssi. The 5' end of this sequence overlaps with the 3' end of AAH41225 and the 3' end of this sequence overlaps with the 5' end of AAH41227. The proteins of the present invention have various potential industrial uses, since the proteins are stable at very high temperatures, some up to 110
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                                                                                             Claim 1; Page 511-606; 1657pp; French
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                                                                                                                                                                                                    (CNRS ) (IFRE-)
                                                                                                                    New nucleotide sequences isolated proteins useful in industry -
                                                                                                                                                   WPI; 2001-126236/14.
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Querellou J,
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Weissenbach
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ID AAH68525 standard;
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US-10-048-197-2 x AAH41226/rev
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analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a nucleic acid described in the exemplification of the invention.

Note: The sequence data for this patent did not form part of the printed
                                                                                           The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. T are useful for identifying the mutation point of a gene derived from mutant of coryneform bacterium, measuring expression amount and
                                                                                                                                                                                                                                                                                                 Nakagawa
Tateishi
                                                                                                                                                                                                                                                                                                                                                                  16-DEC-1999;
07-APR-2000;
03-AUG-2000;
                                                                                                                                                                  Disclosure; SEQ ID NO: 7060; 246pp + Sequence Listing; English.
                                                                                                                                                                                                         Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene
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Note: This patent is in the same patent family as WO200065062, which contains additional sequences as shown in AAB99132-AAB99143, AAH75903-AAH75920 and AAG66436.
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2000JP-0159162.
2000JP-0280988.
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Senoh A, Ikeda M,
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ID ABA72068 standard; DNA; 115
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26-MAY-2000;
30-JUN-2000;
                    The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a single exon nucleic acid probe of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                       27-SEP-2000;
04-OCT-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        European
                                                                                                                                                        Claim 4; SEQ ID NO 20373; 639pp + sequence listing;
                                                                                                                                                                                  Human genome-derived single exon nucleic acid probes useful analyzing gene expression in human fetal liver -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200157277-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 349980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       specification, but was obtained in electronic format directly from the European Patent Office.
 Sequence 115 BP;
                                                                                                                                                                                                                                                                                                                                21-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                 03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                 30-JAN-2001;
                                                                                                                                                                                                                                                                             (MOLE-) MOLECULAR DYNAMICS INC
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                                                                                                                                                                                                                                                    SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              foetal liver single exon nucleic acid probe #20373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      foetal liver; gene expression; single exon nucleic acid probe; ss
                                                                                                                                                                                                                                                    Hanzel
                                                                                                                                                                                                                                                                                                      2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
2000US-0024263.
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2000US-0207456.
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26 A; 35 C; 14 G; 40 T; 0 other;
                                                                                                                                                                                                                                                    Chen W,
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                                                                                                                                                                                                                                                      Rank DR;
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                                                                                                                                                          English.
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seq_documentation_block:
ID AAK20495 standard;
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US-10-048-197-2 x ABA72068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_name: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:AAK20495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Quality: 7.00
Ratio: 1.000
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Align seg 1/1
                                        The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human probes which are derived from genomic sequences expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
                                                                                                                                     Single exon nucleic acid probes for analyzing gene expression in brains -
                                                                                                                                                                                        Penn
                                                                                                                                                                                                                                                                    30-JUN-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                          04-FEB-2000;
26-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                       WO200157275-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; brain expressed exon;
Sequence 115
                               epilepsy and cancers. The present
                                                                                                           Example 4; SEQ ID NO:
                                                                                                                                                                  WPI; 2001-483446/52.
                                                                                                                                                                                                              (MOLE-)
                                                                                                                                                                                                                                    04-OCT-2000;
                                                                                                                                                                                                                                               21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                           30-JAN-2001; 2001WO-US00667
                                                                                                                                                                                                                                                                                                                                                 09-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                 epilepsy; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                            microarray; Alzheimer's
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human brain expressed single exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAK20495 standard; DNA; 115
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2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0632368.
2000US-0236359.
2000US-0236359.
2000US-0236359.
2000US-0236359.
BP;
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26
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                                                                                                           20486; 650pp + Sequence Listing;
                                                                                                                                                                                        Chen W,
35
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Percent Identity: 100.000
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14
                                                                                                                                                                                        Rank DR;
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                               sequence is
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6
T; 0 other;
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                               the probes
                                                                                                                                                                                                                                                                                                                                                                                                                             schizophrenia;
                                                                                                           English.
                                of the
                                                                                                                                             human
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alignment\_block:

Percent Similarity:

Quality: Ratio:

7.00 1.000 100.000

Length: Gaps: Percent Identity:

100.000

07

alignment\_scores:

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seq_documentation_block:
ID AAK46634 standard; DN
AC AAK46634;
XX
AC AAK46634;

XX
DT 06-NOV-2001 (first e
XX
Human bone marrow exp
XX
Human bone marrow exp
XX
Homo sapiens.

XX
Homo sapiens.

XX
PN W0200157276-A2.

XX
PP 30-JAN-2001 2000US-0
PR 26-MAY-2000; 2000US-0
PR 26-MAY-2000; 2000US-0
PR 21-SEP-2000; 2000US-0
PR 03-AUG-2000; 2000US-0
PR 21-SEP-2000; 2000US-0
PR 04-OCT-2000; 2000US-0
PR 11-SEP-2000; 2000US-0
PR 21-SEP-2000; 2000US-0
PR 21-SEP-2000; 2000US-0
PR 11-SEP-2000; 2000US-0
PR 21-SEP-2000; 200US-0
PR 21-SEP-2000; 2000US-0
PR
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US-10-048-197-2 x AAK46634
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Quality:
Ratio:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancer such as lymphoma, leukaemia and myeloma. The present sequence is one of the invention.
                                                     38
                                                                                                      87
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-JAN-2001; 2001WO-US00668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; bone marrow expressed exon; gene expression analysis; microarray; cancer; leukaemia; lymphoma; myeloma; ss.
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                                                                   SerLeuIleIleSerPheLeu 93
                                             TCTTTGATTATTTCCTTTCTC 58
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 genome-derived single exon nucleic acid probes useful
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2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0234687.
2000US-023453.
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Gaps:
Percent Identity:
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XX DX XX
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seq_documentation_block:
ID AAI52470 standard; DNA; 115 BP.
XX
AC AAI52470;
XX
DT 17-OCT-2001 (first entry)
XX
DT 17-OCT-2001 (first entry)
XX
DT 17-OCT-2001 (first entry)
XX
Probe #21156 used to measure gene
KW Probe; microarray; human; placent.
XX
SS Homo sapiens.
XX
PN W0200157272-A2.
XX
PR 30-JAN-2001; 2001WO-US00663.
XX
PF 30-JUN-2000; 2000US-0632366.
PR 26-MAY-2000; 2000US-0632366.
PR 03-AUG-2000; 2000US-0236359.
PR 04-CCT-2000; 2000US-0236359.
PR 03-AUG-2000; 2000US-0236359.
PR 03-AUG-2000; 2000US-0236359.
PR 04-CCT-2000; 2000US-0236359.
PR 04-FEB-2000; 2000US-023663.
PR 03-AUG-2000; 2000US-023663.
PR 04-FEB-2000; 2000US-024687.
PR 04-FEB-2000; 2000US-023663.
PR 04-FEB-2000; 2000US-023663.
PR 0
                                                                                                                          seq_documentation_block:
ID AAC98752 standard;
                                                                                                                                                                                                      seq_name: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:AAC98752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_block:
US-10-048-197-2 x AAI52470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alignment_scores:
Quality:
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      09-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to single exon nucleic acid probes (SENP). The present sequence is one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 115 BP; 26 A; 35 C; 14 G; 40 T; 0 other;
                                                                                                                                                                                                                                                                                            38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 25; SEQ ID No 21156; 654pp; English.
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                                                                                                                                                                                                                                                                               genome-derived single exon nucleic acid
zing gene expression in human placenta -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ratio:
(first entry)
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                                                                                                                          162
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Gaps: 0
Percent Identity: 100.000
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5
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seq_documentation_block:
ID AAS48479 standard;
2×5
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Ratio: 1.000
Percent Similarity: 100.000
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                                                                                                                                                                                                                             US-10-048-197-2 x AAC98752
                                                                                                                                                                                                                                                                                                                                                                                                                                         polynucleotides may be used in diagnostics and research, such as for chromosome identification, and as hybridisation probes. The proteins may also be used to prevent diseases such as neural disorders, immune system disorders, muscular disorders, reproductive disorders, gastrointestinal disorders, wounds, renal disorders, infectious diseases, and cardiovascular disorders. AAC98764 to AAC98772 and AAB54007 represent sequences used in the exemplification of the preser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAC97991 to AAC98763 encode the human colon cancer associated proteins, called human colon cancer antigens, given in AAB53034 to AAB54006. The human colon cancer antigens can have cytostatic, cardioactive, muscular; neuroprotective, immunomodulatory, gynaecological, gastrointestinal, vulnerary, nephrotropic, antlinfective and antibacterial activities, and can be used in gene therapy. The colon cancer antigen polynucleotides, proteins and antibodies to the proteins are useful for the prevention, treatment and diagnosis of colon disorders, such as colon cancer. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Colon cancer associated gene sequences, referred to as colon cancer antigens, useful for the treatment, prevention, and diagnosis of colon disorders such as colon cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   neural disorder; immune system disorder; muscular disorder; reproductive disorder; gastrointestinal disorder; renal disorder; infectious disease; cardiovascular disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                          Sequence 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200055351-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            identification; cytostatic;
immunomodulatory; muscular;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; colon car
identification;
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DB; AAB53995.
                                                                                  /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:AAS48479
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                                                                          US-10-048-197-2 x AAS48479
                                                                                                                       Percent Similarity:
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23-MAY-2000;
26-MAY-2000;
23-OCT-2000;
27-NOV-2000;
22-DEC-2000;
16-FEB-2001;
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                                                                                                                                                                                                                                           oligonucleotide of the invention.
Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electron format directly from WIFO at ftp.wipo.int/pub/published_pct_sequences.
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2000US-242578P.
2000US-242578P.
2000US-257931P.
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2001US-269308P.
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seq_documentation_block:
ID AAS48487 standard; DN
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DT 13-FEB-2002 (first e protain the prota
                                   alignment_block:
US-10-048-197-2 x AAS48487
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, Pseudomonas aeruginosa and Enterococcus faccalis. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen compounds are required for cell proliferation in a wide variety of organisms. The present sequence is an antisense
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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the
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alignment_scores:
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        Percent Similarity:
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AAH84463 standard; DNA; 200 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel nucleic acids that inhibit Escherichia coli proliferation, useful for screening for homologous genes and for designing expression vectors
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US-10-048-197-2 x AAH84463/rev

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seq_documentation_block:
ID AAC82842 standard; cD
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AC AAC82842;
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CAC AAC82842;
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DT 20-MAR-2001 (first e
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LMTF; lipid metaboli;
KW antiarteriosclerosis; cir;
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AC AMS musculus.
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AC AMS musculus.
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DA W0200073443-A1.
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PN W020007443-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This invention describes a novel purified mammalian nucleotide sequence (I) encoding a lipid metabolism transcription factor (LMTF) which has cytostatic, hepatotropic, antiarteriosclerotic and nephrotropic activity. The probe hybridizing (I) is useful for detecting a mammalian nucleic acid sequence in a sample. (I) is useful to screen a library of molecules to identify at least a molecule specific to (I), comprising combining (I) with a library of molecules under conditions of binding and detecting the specific binding. LMTF is useful for treating or preventing a condition associated with altered expression or activity of the protein, which includes cell proliferation disorders such as atherosclerosis, cirrhosis,
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/ Ggn2_6/ptodata/2/ina/6B_COMB.seq:US-09-058-260-13-
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/ Ggn2_6/ptodata/2/ina/5A_COMB.seq:US-08-619-554-1-
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/ Ggn2_6/ptodata/2/ina/5A_COMB.seq:US-08-619-554-1-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Database: Issued_Patents_NA:*
Database sequences: 383533
Database length: 122816752
Search time (sec): 77.900000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query length: 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Date: Sep 18, 2002 10:19 AM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OM of: US-10-048-197-2 to: Issued_Patents_NA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query: US-10-048-197-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Search information block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /cgn2_6/ptodata/2/1na/6A_COMB.seq:US-08-961-083-7 -
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/cgn2_6/ptodata/2/1na/5B_COMB.seq:US-08-932-978-1-
/cgn2_6/ptodata/2/1na/5A_COMB.seq:US-08-367-198A-1-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Command line parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -HEAPSIZE-500 -MINLEN-0 -MAXLEN-2000000000
-USER-US10048197_@CGN1_1_74 -NCPU-6 -ICPU-3 -LONGLOG
-DEV_TIMEOUT-120 -WARN_TIMEOUT-30 -NO_XLPXY -WAIT -THREADS-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -DELOP=6.000 -DELEXT=7.000 -START=1 -MATRIX=011go
-TRANS=human40.cd1 -LIST=45 -DOCALIGN=200 -THR_SCORE=quality
-THR_MIN=1 -ALIGN=40 -MODE=LOCAL -OUTFNT=pfs -NORM-ext
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-O=/Cgn2_1/USFT0_spco1/US10048197/runat_17092002_135957_23562/app_query.fasta_1.168
-DB-ISSued_Patents_NA -QEMTF-fastap -SUFFIX-ol1.rni -GAPOP-4.500
-GAPEXT-0.050 -MINMATCH-0.100 -LOOPCL-0.000 -LOOPEXT-0.000
-OGAPOP-4.500 -QGAPEXT-0.050 -XGAPOP-60.000 -XGAPEXT-60.000
-FGAPOP-6.000 -FGAPEXT-7.000 -YGAPOP-60.000 -YGAPEXT-60.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         XGAPOP and YGAPOP must be equal. Assuming YGAPOP-XGAPOP-60.000 XGAPEXT and YGAPEXT must be equal. Assuming YGAPEXT-XGAPEXT-60.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    out_format : pfs
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95.35 1.3e-
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Patent No.
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alignment_block:
US-10-048-197-2 x US-08-411-706-3/rev
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/cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-004-139B-10-
                                                                                                    Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 885 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: FI 9:
FILING DATE: 06-0CT-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: 312/474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA: APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Meyers, Thomas C. REGISTRATION NUMBER: 36, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: Illinois COUNTRY: United States of America ZIP: 60606-6402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 6300 (CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE:
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    Application US/08411706
    5789193

                                                                                                                                                                      Quality:
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TYPE: Floppy disk
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X 2180-1B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PatentIn Release #1.0, Version #1.25
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seq_documentation_block:
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US-10-048-197-2 x US-09-318-978-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; PUBLICATION INFORMATION: US-09-318-978-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-318-978-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_documentation_block:
    Sequence 15, Application US/09318978A
    Patent No. 6245526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Align seg 1/1 to: US-09-318-978-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
                                                                                                                                                                                                                                                   Sequence 1, Application US/08747221B

Patent No. 6063610

GENERAL INFORMATION:
APPLICANT: Silver, Gary W.
APPLICANT: Wisnewski, Nancy
TITLE OF INVENTION: No. 6063610el Carboxylesterase Nucleic Acid
TITLE OF INVENTION: Molecules, Proteins and Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Align seg 1/1 to reverse of: US-08-411-706-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/318,978A CURRENT FILING DATE: 1999-05-26 NUMBER OF SEQ ID NOS: 27 SOFTWARE: PERL Program SEQ ID NO 15 LENGTH: 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Yue, Henry
APPLICANT: Kaser, Matthew, R.
APPLICANT: Baughn, Mariah, R.
TITLE OF INVENTION: LIPID METABOLISM TRANSCRIPTION FACTOR
FILE REFERENCE: PC-0004 US
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: unsure
LOCATION: 45
OTHER INFORMATION: a or g or c or t, unknown, or other
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OTHER INFORMATION: 701252210H1
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ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
                                                                                                                                                                       NUMBER OF SEQUENCES: 66
CORRESONDENCE ADDRESSE: Carol Talkington Verser,
ADDRESSEE: Heska Corporation
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                                                                                                                               STREET: 1825 Sharp Point Drive CITY: Fort Collins
                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACAGCACTGTTGGTAACCGGT 105
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Ratio:
                                                                    80525
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Gaps: 0
Percent Identity: 100.000
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FEATURE:

NAME/KEY:

LOCATION:

US-08-747-221B-1
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US-10-048-197-2 x US-08-747-221B-1/rev
                                                                                                                                                                                                                                                                                                                                                                                                                    seq_documentation_block:
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Ratio: 1.000
Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                  Patent No.
                                                                                                                                                                                                                                                                                                                                                                                Sequence 3, Application US/08747221B Patent No. 6063610
                                                                                                                                                                                                                                                          APPLICANT: Silver, Gary
APPLICANT: Wisnewski, I
TITLE OF INVENTION: MO
TITLE OF INVENTION: MO
NUMBER OF SEQUENCES: 61
                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO: 1:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect for Windows, Version 7.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION:
FEATURE:
NAME/KEY:
                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                156 TTATCATTAATCATTTCCTTC 136
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NAME/KEY:
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REFERENCE/DOCKET NUMBER: FC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect for Windows, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/747,221B
FILING DATE: No. 6063610ember 12, 1996
CLASSIFICATION: 435
CCLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION: NAME: Verser, Carol Talk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: cDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    86 LeuSerLeuIleIleSerPhe 92
                                                                                                                                            STREET: 1825 Sharp Point Drive
CITY: Fort Collins
STATE: Colorado
                                                                                                       ZIP: 80525
                                                                                                                        COUNTRY:
                                                                                                                                                                                                     ADDRESSEE: Carol Talkington Verser, Ph.D. ADDRESSEE: Heska Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Verser, Carol Talkington REGISTRATION NUMBER: 37,459
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92..400
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332
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275, 329
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218
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                                                                                                                                                                                                                                                                                                                     Nancy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Identity: 100.000
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ATTORNEY/AGENT INFORMATION:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: FILING DATE: No. 60 CLASSIFICATION:

No. 435

6063610ember 12, 1996 US/08/747,221B

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alignment_scores:
Quality:
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US-10-048-197-2 x US-08-747-221B-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_name: /cgn2_6/ptodata/2/1na/6B_COMB.seq:US-09-005-051-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Quality: 7.00
Ratio: 1.000
Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/09005051 Patent No. 6291222
CLASSIFICATION:
CLASSIFICATION:
PRIOR APPLICATION NUMBER: 08/747,221
APPLICATION NUMBER: 08/747,221
FILING DATE: NO. 629122ember 12, 19
ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: FC-1
TELECOMMUNICATION INFORMATION:
TELECPHONE: 970/493-7272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: 970/493-7272
TELEFAX: 970/494-9505
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: Windows 95 SOFTWARE: WordPerfect for Windows, CURRENT APPLICATION DATA:
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REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: FC-1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Wisnewski, Nancy TITLE OF INVENTION: No. 6291222el Carboxylesterase Nucleic TITLE OF INVENTION: Molecules, Proteins and Uses Thereof NUMBER OF SEQUENCES: 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Carol Talkington Verser, Ph.D. ADDRESSEE: Heska Corporation STREET: 1825 Sharp Point Drive CITY: Fort Collins STATE: Colorado
                                                                                                                                                                                                                            APPLICATION NUMBER: US/09/005,051 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
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alignment_block:
US-10-048-197-2 x US-09-005-051-1/rev
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Quality:
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; LOCATION:
US-09-005-051-1
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Percent Similarity: 100.000
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SEQUENCE CHARACTERISTICS:
LENGTH: 401 nucleotides
TYPE: nucleic acid
STRANDENNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3, Application US/09005051
Patent No. 6291222
GENERAL INFORMATION:
APPLICANT: Silver, Gary W.
APPLICANT: Wisnewski, Nancy
                                                                                                                                                                                                                   ZIP: 80525
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPorfect for Windows,
CURRENT APPLICATION DATA:
NAME: Verser, Carol Talkington REGISTRATION NUMBER: 37,459 REFERENCE/DOCKET NUMBER: FC-1 TELECOMMUNICATION INFORMATION: TELEPHONE: 970/493-7272
                                                                                      APPLICATION NUMBER: 08/747,22: FILING DATE: NO. 6291222ember ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
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NAME/KEY:
                                                                                                                                              PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: No. 6291222el Carboxylesterase Nucleic Acid
TITLE OF INVENTION: Molecules, Proteins and Uses Thereof
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                                                                                                                                                                                                                                                                                                                                                             STREET: 1825 Snarp
CITY: Fort Collins
STATE: Colorado
                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Carol Talkington Verser, Ph.D. ADDRESSEE: Heska Corporation
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218
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332
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275, 329
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                                                                                                                              08/747,221
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                                                                                                         12,
                                                                                                           1996
                                                                                                                                                                                                                                        Version
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seq_documentation_block:
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US-10-048-197-2 x US-09-005-051-3
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Sequence 4, Application US/08367198A
Patent No. 5627049
GENERAL INFORMATION:
APPLICANT: Menart, Sandrine
APPLICANT: Bolottn, Monique
TITLE OF INVENTION: K. lactis RP28 Ribosomal Protein Gene
TITLE OF INVENTION: Promoter and Use Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Align seg 1/1 to: US-09-005-051-3
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                                                                                                               TELEFAX: (610)454-380 INFORMATION FOR SEQ ID NO:
                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 549 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
              MOLECULE TYPE:
ANTI-SENSE:
                                                                                                                                            TELEPHONE: (610)454-3839
                                                                                                                                                                                                                             APPLICATION NUMBER: FR 92/08429
FILING DATE: 08-JUL-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                           APPLICATION NUMBER: WO PCT/FR93/00695
FILING DATE: 06-JUL-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/367,198A
FILING DATE: 01-FEB-1995
                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
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                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               86 LeuSerLeuIleIleSerPhe 92
                                          STRANDEDNESS:
                                                                                                                                                                             REGISTRATION NUMBER: 38
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
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                                                                                                                                                                                                                      NAME:
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STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19426-0107
                                                          nucleic acid
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500 Arcola Road, 3C43
                                                                                                                               (610)454-3808
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Gaps: 0
Percent Identity: 100.000
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alignment_block:
US-10-048-197-2 x US-08-932-978-1/rev
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Quality:
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US-08-932-978-1
Align seg 1/1 to reverse of: US-08-932-978-1 from: 1
                                                                            Quality: 7.00
Ratio: 1.000
Percent Similarity: 100.000
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US-10-048-197-2 x US-08-367-198A-4/rev
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Ratio: 1.000
Percent Similarity: 100.000
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION: TELEPHONE: 215-994-2252
                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION: NAME: Dickinson, Todd O
                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 536 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
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MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Zalacain, Magdalena, APPLICANT: Brown, James R. TITLE OF INVENTION: NOVEL PhoH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241 CATCACATCAGACTGACGATC 221
                                                                                                                                                                                                        TYPE: nuclei
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                            NAME: Dickinson, Todd Q
REGISTRATION NUMBER: 28,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                    TELEFAX:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE:
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OPERATING SYSTEM:
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                                                                                                                                                                                                                    nucleic acid
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Gaps:
Percent Identity:
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alignment_block:
US-10-048-197-2 x US-08-367-198A-1/rev
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Quality:
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Ratio: 1.000
Percent Similarity: 100.000
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NAME: Smith, Julie K.
REGISTRATION NUMBER: 38,619
REFERENCE/DOCKET NUMBER: ST92045-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610)454-3839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 06-JUL-1993 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
577 CATCACATCAGACTGACGATC 557
                                                                                                                                                                                                                                                                                                      FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
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CITY: Collegeville
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               4 HisHisIleArgLeuThrIle 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/0 FILING DATE: 01-FEB-1995
                                                                                                                                                                                                                                                                                                                      ORGANISM: Kluyveromyces lactis
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                                                                                                                                                                                                                                                                                                                                                                                                                                     970 base pairs
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Bolotin, Monique
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TD NO: 1:
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Promoter and Use Thereof
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Percent Identity: 100.000
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seq_documentation_block:
    Sequence 9, Application US/08684862
    Patent No. 5759541
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US-08-961-083-7
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Percent Similarity:
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Patent No. 6159469
GENERAL INFORMATION:
                                APPLICANT: Bach, Alfred
APPLICANT: Hillen, Heinz
APPLICANT: Bialojan, Siegfrie
TITLE OF INVENTION: No. 57595
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 14
                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (301) 309-851:
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 985 base pairs
TYPE: nucleic acid
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CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                     268 ATTATTAAGGGCAAAACCAAC 248
                                                                                                                                                                                                                                                                                          42 IleIleLysGlyLysThrAsn 48
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NUMBER OF SEQUENCES:
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OPERATING SYSTEM:
SOFTWARE: ASCII 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 9410 Key West Avenue CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
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Keil & Weinkauf
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                                                                    No. 5759541el Proteins,
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Percent Identity:
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OTHER INFORMATION: th;
OTHER INFORMATION: courselosses
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US-10-048-197-2 x US-08-684-862-9/rev
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Quality:
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Ratio: 1.000
Percent Similarity: 100.000
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FILING DATE: 30-DEC-1992
APPLICATION NUMBER: PCT/EP91/01361
FILING DATE: 19-UUL-1991
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGIH: 1333 base pairs
TYPE: nucleic acid
STRANDENMES: 6:61
                                                                                                                                                                                                                                                                                                                                           Patent No.
                 CURRENT APPLICATION NUMBER: US/09/058, 260B CURRENT FILING DATE: 1999-04-10 EARLIER APPLICATION NUMBER: 60/001, 995 EARLIER FILING DATE: 1996-08-07 EARLIER APPLICATION NUMBER: 60/009, 704 EARLIER FILING DATE: 1996-01-11
                                                                                                                                             APPLICANT: Allen, Larry
APPLICANT: Aikens, John
APPLICANT: Aikens, John
APPLICANT: Fonstein, Michael
APPLICANT: Vonstein, Veronika
APPLICANT: Demirjian, David
APPLICANT: Casadaban, Malcolm
TITLE OF INVENTION: Stable Biocatalysts for Ester Hydrolysis
FILE REFERENCE: 95-963-H
EARLIER APPLICATION NUMBER: 60/019,580
                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: 1
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APPLICATION NUMBER: US/08/684,862
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COMPUTER: IBM AT-compatible, 80286 processor
OPERATING SYSTEM: MS-DOS version 5.0
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                                                                                                                                                                                                                                                                                                                 INFORMATION:
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linear
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CURRENT APPLICATION NUMBER: US/09/058,260B
CURRENT FILING DATE: 1999-04-10
EARLIER APPLICATION NUMBER: 60/001,995
EARLIER FILING DATE: 1996-08-07
EARLIER APPLICATION NUMBER: 60/009,704
EARLIER APPLICATION NUMBER: 60/019,580
EARLIER APPLICATION NUMBER: 60/019,580
EARLIER FILING DATE: 1996-06-12
EARLIER FILING DATE: 1996-08-12
EARLIER FILING DATE: 1996-08-08
EARLIER FILING DATE: 1996-08-08
EARLIER FILING DATE: 1997-01-10
EARLIER APPLICATION NUMBER: 08/781,802
EARLIER APPLICATION NUMBER: 08/781,802
EARLIER APPLICATION NUMBER: 08/781,802
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EARLIER APPLICATION NUMBER: 08/78
EARLIER FILING DATE: 1997-01-10
EARLIER APPLICATION NUMBER: 08/82
EARLIER FILING DATE: 1997-04-11
NUMBER OF SEQ ID NOS: 37
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 13
LENGTH: 1699
TYPE: DNA
ORGANISM: Artificial Sequence
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; LOCATION: (92)..(1594)
US-09-058-260-13
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                                                                                                       EARLIER APPLICATION NUMBER: 08/827,810
EARLIER FILING DATE: 1997-04-11
NUMBER OF SEQ ID NOS: 37
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 21
LENGTH: 1753
TYPE: DNA
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Ratio: 1.000
Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Fonstein, Michael
APPLICANT: Vonstein, Veronika
APPLICANT: Demirjian, David
APPLICANT: Casadaban, Malcolm
TITLE OF INVENTION: Stable Biocatalysts for Ester Hydrolysis
FILE REFERENCE: 95-963-H
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OTHER INFORMATION: Description of Artificial Sequence:cloned esterase OTHER INFORMATION: gene from bacteria E013
                                                                       ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Aikens, John
                                                             FEATURE:
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EARLIER APPLICATION NUMBER: 08/
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Percent Identity:
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; FEATURE: ; NAME/KEY: CDS ; LOCATION: (128)..(1630) US-09-058-260-21

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alignment_scores: 7.00
Quality: 7.00
Ratio: 1.000
Percent Similarity: 100.000
                                       alignment_block:
US-10-048-197-2 x US-09-058-260-31/rev
                                                                                                                  alignment_scores: 7.00
Quality: 7.00
Ratio: 1.000
Percent Similarity: 100.000
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US-10-048-197-2 x US-09-058-260-21/rev
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; LOCATION: (130)..(1632)
US-09-058-260-31
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EARLIER APPLICATION NUMBER: 60/001,995
EARLIER APPLICATION NUMBER: 60/001,995
EARLIER FILLING DATE: 1996-08-07
EARLIER FILLING DATE: 1996-08-07
EARLIER FILLING DATE: 1996-01-11
EARLIER FILLING DATE: 1996-06-12
EARLIER FILLING DATE: 1996-06-12
EARLIER FILLING DATE: 1996-06-12
EARLIER FILLING DATE: 1996-08-08
EARLIER FILLING DATE: 1996-08-08
EARLIER FILLING DATE: 1997-01-10
EARLIER APPLICATION NUMBER: 08/781,802
EARLIER APPLICATION NUMBER: 08/781,802
EARLIER FILLING DATE: 1997-01-10
EARLIER FILLING DATE: 1997-04-11
NUMBER: 08/827,810
EARLIER FILLING DATE: 1997-04-11
NUMBER: DATE: 1997-04-11
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Align seg 1/1 to reverse of: US-09-058-260-31
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SEQ ID NO 31
LENGTH: 1756
TYPE: DNA
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APPLICANT: Vonstein, Veronika
APPLICANT: Demirjian, David
APPLICANT: Casadaban, Malcolm
TITLE OF INVENTION: Stable Biocatalysts for Ester Hydrolysis
FILE REFERENCE: 95-963-H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Allen, Larry
APPLICANT: Alkens, John
APPLICANT: Fonstein, Mi
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Gaps:
Percent Identity:
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Percent Identity:
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from:
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alignment_block:
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                                                                                                                                                                                                            seq_documentation_block:
                                                                                                                                                                                                                                                    seq_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-058-260-3
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US-09-058-260-23
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CURRENT FILING DATE: 1999-04-10
EARLIER APPLICATION NUMBER: 60/001,995
EARLIER FILING DATE: 1996-08-07
EARLIER APPLICATION NUMBER: 60/009,704
EARLIER FILING DATE: 1996-01-11
EARLIER FILING DATE: 1996-01-11
EARLIER APPLICATION NUMBER: 60/019,580
EARLIER FILING DATE: 1996-08-08
EARLIER APPLICATION NUMBER: 08/694,078
EARLIER APPLICATION NUMBER: 08/694,078
                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-048-197-2 x US-09-058-260-23/rev
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Ratio: 1.000
Percent Similarity: 100.000
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Patent No. 6218167
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LENGTH: 1776
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EARLIER FILING DATE: 1997-01-10
EARLIER APPLICATION NUMBER: 08/827,810
EARLIER FILING DATE: 1997-04-11
NUMBER OF SEQ ID NOS: 37
SOFTMARE: Patentin Ver. 2.0
                                             APPLICANT: Fonstein, Michael APPLICANT: Vonstein, Veronika
                                                                                           APPLICANT: Allen, Larry APPLICANT: Aikens, John
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APPLICANT: Casadaban, Malcolm
TITLE OF INVENTION: Stable Biocatalysts for Ester Hydrolysis
FILE REFERENCE: 95-963-H
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                          APPLICANT:
                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Description of Artificial Sequence:cloned esterase OTHER INFORMATION: gene from bacteria E015
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Demirjian, David
Casadaban, Malcolm
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Vonstein, Veronika
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seq_documentation_block:
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US-10-048-197-2 x US-09-058-260-3/rev
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; LOCATION: (211)..(1713)
US-09-058-260-3
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Ratio: 1.000
Percent Similarity: 100.000
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EARLIER FILING DATE: 1996-08-07
EARLIER APPLICATION NUMBER: 60/009,704
EARLIER FILING DATE: 1996-01-11
EARLIER APPLICATION NUMBER: 60/019,580
EARLIER FILING DATE: 1996-06-12
EARLIER FILING DATE: 1996-08-08
EARLIER FILING DATE: 1996-08-08
EARLIER FILING DATE: 1997-01-10
EARLIER APPLICATION NUMBER: 08/781,802
EARLIER FILING DATE: 1997-01-10
EARLIER FILING DATE: 1997-04-11
NUMBER OF SEQ ID NOS: 37
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                                          EARLIER APPLICATION NUMBER: 60/019,580 EARLIER FILING DATE: 1996-06-12 EARLIER APPLICATION NUMBER: 08/694,078 EARLIER FILING DATE: 1996-08-08 EARLIER APPLICATION NUMBER: 08/781,802 EARLIER FILING DATE: 1997-01-10
EARLIER
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APPLICANT: Vonstein, Veronika
APPLICANT: Demirjian, David
APPLICANT: Casadaban, Malcolm
TITLE OF INVENTION: Stable Biocatalysts for Ester Hydrolysis
FILE REFERENCE: 95-963-H
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ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Description of Artificial Sequence:cloned esterase OTHER INFORMATION: gene from bacteria E009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OF INVENTION: Stable Biocatalysts for Ester Hydrolysis REFERENCE: 95-963-H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GAAATTAGCTCCCGCTTCGGA 1512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GluIleSerSerArgPheGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION:
           FILING DATE: 1997-01-10
APPLICATION NUMBER: 08/827,810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /, Application US/09058260B 6218167
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; FEATURE:
; NAME/KEY: CDS
; LOCATION: (197)..(1699)
US-09-058-260-5
                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/058, 260B
CURRENT FILING DATE: 1999-04-10
EARLIER APPLICATION NUMBER: 60/001,995
EARLIER APPLICATION NUMBER: 60/009,704
EARLIER APPLICATION NUMBER: 60/009,704
EARLIER FILING DATE: 1996-06-12
EARLIER APPLICATION NUMBER: 60/019,580
EARLIER APPLICATION NUMBER: 60/019,580
EARLIER APPLICATION NUMBER: 08/694,078
EARLIER APPLICATION NUMBER: 08/694,078
EARLIER FILING DATE: 1996-08-08
EARLIER FILING DATE: 1996-08-08
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US-10-048-197-2 x US-09-058-260-17/rev
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; LOCATION: (127)..(1581)
US-09-058-260-17
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Ratio: 1.000
Percent Similarity: 100.000
                                                                                                                                                                                                                            SOFTWARE: PatentIn Ver.
SEQ ID NO 5
LENGTH: 1952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Align seg 1/1 to reverse of: US-09-058-260-17
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SOFTWARE: PatentIn Ver. :
SEQ ID NO 17
LENGTH: 1925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 5, Application US/09058260B Patent No. 6218167
                                                                                                                                                                                                                                                                                                 EARLIER APPLICATION NUMBER: 08/827,810 EARLIER FILING DATE: 1997-04-11 NUMBER OF SEQ ID NOS: 37
                                                                                                                                                                                                                                                                                                                                                                              EARLIER APPLICATION NUMBER: 08/781,802
EARLIER FILING DATE: 1997-01-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Casadaban, Malcolm
TIPLE OF INVENTION: Stable Biocatalysts for Ester Hydrolysis
FILE REFERENCE: 95-963-H
                                                                                               OTHER INFORMATION: Description of Artificial Sequence:cloned esterase OTHER INFORMATION: gene from bacteria E011
                                                                                                                                                    ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Demirjian,
APPLICANT: Casadaban,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Fonstein, Michael APPLICANT: Vonstein, Veronika
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Aikens, John
                                                                                                                                                                                                       TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Allen, Larry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1400 GAAATTAGCTCCCGCTTCGGA 1380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Description of Artificial Sequence:cloned esterase OTHER INFORMATION: gene from bacteria E008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51 GluIleSerSerArgPheGly 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps:
Percent Identity:
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100.000
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alignment\_scores

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alignment_block:
US-10-048-197-2 x US-09-263-023-3
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; LOCATION: (390)...(1841)
US-09-263-023-3
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US-10-048-197-2 x US-09-058-260-5/rev
                                                                                                                                                                                                                                      seq_documentation_block:
                                                                                                                                                                                                                                                                                   seq_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-08-894-997-49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_scores:
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Ratio: 1.000
Percent Similarity: 100.000
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                                                         Sequence 49, Application US/08894997A
Patent No. 6270990
GENERAL INFORMATION:
APPLICANT: Anderson, David J
APPLICANT: Schoenherr, Christopher J
TITLE OF INVENTION: NEURON-RESTRICTIVE SILENCER FACTOR
FILE REFERENCE: 17810-502 URSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: MUTAMATEU, HIDEKI
APPLICANT: KADOMALEU, Kenji
APPLICANT: KADOMALEU, Kenji
APPLICANT: KADOMALEU, Kenji
APPLICANT: HADUCHI, OSAMI
APPLICANT: HADUCHI, OSAMI
TITLE OF INVENTION: POLYPEPTIDE OF N-ACETYLGLUCOSAMINE-6-0-SULFOTRANSFERASE AND
TITLE OF INVENTION: DNA ENCODING THE SAME
FILLE REFERENCE: TOYAM41,001AUS
CURRENT APPLICATION NUMBER: US/09/263,023
CURRENT FILING DATE: 1999-03-05
EARLIER FILING DATE: 1999-03-05
EARLIER APPLICATION NUMBER: UF 10-54007
EARLIER APPLICATION NUMBER: UF 10-177844
ERALIER FILING DATE: 1998-06-24
                   CURRENT APPLICATION NUMBER: US/08/894,997A CURRENT FILING DATE: 1998-01-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 10
EARLIER APPLICATION NUMBER: PCT/US96/02817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1518
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ENGTH:
                                                                                                                                                                                                                                                                                                                                  614 TCCGCACTCCTTACCGCCCTC 634
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                                                                                                                                                                                                                                                                                                                                                                                 11 SerAlaLeuLeuThrAlaLeu 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GAAATTAGCTCCCGCTTCGGA 1498
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Gaps: 0
Percent Identity: 100.000
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Gaps: 0
Percent Identity: 100.000
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alignment_block:
US-10-048-197-2 x US-08-894-997-49/rev
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; LOCATION: (1)..(4057)
; OTHER INFORMATION: Human NSRF
US-08-894-997-49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_name: /cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-781-802-5
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Ratio: 1.000
Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  šequence 5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: AIKENS, John
APPLICANT: FONSTEIN, Michael
APPLICANT: VONSTEIN, Veronika
APPLICANT: DEMIRIJAN, DAVId
APPLICANT: CASADABAN, Malcolm
TITLE OF INVENTION: Stable Bioc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EARLIER FILING DATE: 1996-03-01
EARLIER APPLICATION NUMBER: 08/398,590
EARLIER FILING DATE: 1995-03-03
NUMBER OF SEQ ID NOS: 55
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TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4011 AAAGGAAAAACAAACAAACAA 3991
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                                                 CLASSIELCATION DATA APPLICATION NUMBER: US 60/019,580 APPLICATION NUMBER: US 60/019,580 FILING DATE: 12-JUN-1996 PRIOR APPLICATION NUMBER: US 60/009,704 FILING DATE: 11-JAN-1996
                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                    PRIOR APPLICATION DATA:
                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/694,078
FILING DATE: 07-AUG-1996
                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 60606
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 1
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                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/781,802 FILING DATE: 10-JAN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Chicago
STATE: Illinois
                                                                                                                                                                                  CLASSIFICATION: 536
                                                                                                                                                                                                                                                            CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
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MBER: US 60/001,995
01-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Stable Biocatalysts for Ester Hydrolysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps:
Percent Identity:
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ATTORNEY/AGENT INFORMATION

REGISTRATION NUMBER:

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alignment_block:
US-10-048-197-2 x US-08-781-802-5/rev
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Quality:
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Sequence 5, Application US/08694078
Patent No. 6218163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1518 GAAATTAGCTCCCGCTTCGGA 1498
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/019,580
FILING DATE: 12-JUN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: DEMIRJIAN, David
APPLICANT: CASADABAN, Malcolm
TITLE OF INVENTION: Stable Biocatalysts for Ester Hydrolysis
                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 37, 293
REFERENCE/DOCKET NUMBER: 95
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-913-0001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
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                                                                                                                                                                                                                                                                                                           STREET: 300 S. CITY: Chicago STATE: Illinoi
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LOCATION:
                                                                         CLASSIFICATION:
                                                                                        APPLICATION NUMBER: US/08/694,078 FILING DATE: 07-AUG-1996
                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: /note= "E011 sequence of longest
OTHER INFORMATION: open reading frame; other possible start codons ATG/met4;
OTHER INFORMATION: TTG/leu7; GTG/val8; GTG/val15; GTG/val36; ATG/met62"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: CDS
LOCATION: 197..1699
OTHER INFORMATION: OTHER INFORMATION: O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: sing
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 4090 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GluIleSerSerArgPheGly 57
                                                                                                                                                                                                                                                                   60606
                                                                                                                                                                                                                                                                                                           Illinois
                                                                                                                                                                                                                                                                                                                                                 E: McDonnell Boehnen Hulbert & Berghoff, Ltd. 300 S. Wacker Drive 7th Floor
                                                                                                                                                                                                                                                                                       USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FONSTEIN, Michael
VONSTEIN, Veronika
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ALLEN, Larry
AIKENS, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mat_peptide
197..1699
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1.000
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alignment_block:
US-10-048-197-2 x US-08-694-078-5/rev
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; LOCATION:
US-08-694-078-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-08-485-355B-45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Align seg 1/1 to reverse of: US-08-694-078-5 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Quality: 7.00
Ratio: 1.000
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 45, Application US/08485355B
Patent No. 6177075
GENERAL INFORMATION:
APPLICANT: Christian, P. D., Gordon, K. H.J., Hanzlik, T. N.
TITLE OF INVENTION: Insect Viruses and Their Uses in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 4090 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1518 GAAATTAGCTCCCGCTTCGGA 1498
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REFERENCE/DOCKET NUMBER: 95
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-913-0001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 60/001,995
FILING DATE: 07-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Chao, Mark
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: CDS
LOCATION: 197..1699
OTHER INFORMATION: //
OTHER INFORMATION: OPERING OTHER INFORMATION: TO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/009,704
FILING DATE: 10-JAN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                51 GluIleSerSerArgPheGly 57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS: single
                     COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,355B
FILING DATE: 07-Jun-1995
CLASSIFICATION: <Unknown>
                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:

ADDRESSEE: Flehr Hohbach Test Albritton & Herbert LLP
STREET: Four Embarcadero Center, Suite 3400
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                            COUNTRY: United States ZIP: 94111-4187
                                                                                                                                                                                                                                                                      CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         312-913-0002
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197..1699
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open reading frame; other possible start codons ATG/met4;
TTG/leu7; GTG/val8; GTG/val15; GTG/val36; ATG/met62"
                                                                                                                                                                                                                                                                                                                                                                                              Protecting Plants: 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps: 0
Percent Identity: 100.000
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APPLICATION NUMBER: US 08/440,522 FILING DATE: 12-MAY-1995 APPLICATION NUMBER: US 08/089,372 FILING DATE: 08-JUL-1993

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NAME/KEY: CDS

LOCATION: 4944..5162

SEQUENCE DESCRIPTION: SEQ ID NO: 45:

US-08-485-355B-45
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US-10-048-197-2 x US-08-485-3558-45
                                                                                                                                                                                                                                                                                                                                                                                                                            seq_documentation_block:
;Patent No. 5223424
;Patent No. 5223424
;RICHARD D. TITLE OF INVENTION: ATTENUATED HERPESVIRUSES AND;HERPESVIRUSES WHICH INCLUDE FOREIGN DNA ENCODING AN AMINO;ACID SEQUENCE
5223424-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_name: /cgn2_6/ptodata/2/ina/backfiles1.seq:5223424-5
                  SEQ ID NO:5:
LENGTH: 5379
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                                                        NUMBER OF SEQUENCES: 16
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/22:
FILING DATE: 27-JUL-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 78,519
FILING DATE: 20-NOV-1986
APPLICATION NUMBER: 933 107
FILING DATE: 20-NOV-1986
APPLICATION NUMBER: 902,887
FILING DATE: 02-SEP-1986
APPLICATION NUMBER: 887,140
FILING DATE: 17-JUL-1986
APPLICATION NUMBER: 823,102
FILING DATE: 27-JAN-1986
APPLICATION NUMBER: 773,430
FILING DATE: 27-JAN-1986
APPLICATION NUMBER: 773,430
FILING DATE: 06-SEP-1985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 5368 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: AU PL4081/92
FILING DATE: 14-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME: Trecartin, Richard F.
REGISTRATION NUMBER: 31,801
REFERENCE/DOCKET NUMBER: A-58631-2/RFT/DSS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: DNA
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Gaps: 0
Percent Identity: 100.000
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-477-451-9
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US-10-048-197-2 x 5223424-5/rev
                                                                                                                                                                                         alignment_block:
US-10-048-197-2 x US-08-477-451-9
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Quality:
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seq_documentation_block:
                                  seq_name: /cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-477-451-13
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Ratio: 1.000
Percent Similarity: 100.000
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Ratio: 1.000
Percent Similarity: 100.000
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                                                                                                                                                       Align seg 1/1 to: US-08-477-451-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: MCClung, Barbara G.
REFERENCE/DOCKET NUMBER: 33,113
REFERENCE/DOCKET NUMBER: 0335
TELECOMMUNICATION INFORMATION:
TELEPHONE: 510-601-2708
TELEPHONE: 510-655-3542
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 9, Application US/08477451 Patent No. 5928865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Covacci, Antonello
TITLE OF INVENTION: Helicobact
NUMBER OF SEQUENCES: 46
                                                                        COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 94608-2916
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              733 TTAACAATAAGTGCGTTGTTA 713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Emeryville STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8 LeuThrIleSerAlaLeuLeu 14
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                                                                                                                                                                                                                                                                                                                                                                                         DNA (genomic)
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Gaps: 0
Percent Identity: 100.000
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Gaps: 0
Percent Identity: 100.000
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                                                                                                                                                           from:
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alignment_block:
US-10-048-197-2 x US-08-477-451-13/rev
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; MOLECULE TYPE: DNA (genomic) US-08-477-451-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 5599 base pairs
TYPE: nucleic acid
TYPE: nucleic single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ratio: 1.000
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1 to reverse of: US-08-477-451-13
                                                                                                                                                                                                                                                       Sequence 4, Application US/08470260 Patent No. 6077706 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 13, Application US/08477451 Patent No. 5928865
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                                                                                                                                                                                                                        APPLICANT:
APPLICANT:
                                                                                                             APPLICANT: Telford, John
APPLICANT: Macchia, Glovanni
APPLICANT: Rappuoli, Rino
TITLE OF INVENTION: Helicobacter
TITLE OF INVENTION: for Vaccines
NUMBER OF SEQUENCES: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/477,451

FILING DATE: 07-UN-1995

CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: MCClung, Barbara G.
REGISTRATION NUMBER: 33,113
REFERENCE/DOCKET NUMBER: 0335.002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 510-601-2708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                 85 IleLeuSerLeuIleIleSer 91
         STREET: 4560 Horton Street
CITY: Emeryville
STATE: California
COUNTRY:
                                                                      ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                              ATTTTGAGCTTGATCATTTCG 2247
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                                                                                                                                                                                                 Covacci,
Bugnoli,
Telford,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
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                                                                    Chiron Corporation
                                                                                                                                                                                                                        Massimo
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Helicobacter Pylori Cagi Region
                                                                                                                                                                                                                                           Antonello
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length: 7
Gaps: 0
Percent Identity: 100.000
                                                                                                                          Pylori Proteins and Diagnostics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        from:
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; TYPE: DNA
; ORGANISM: Helicobacter pylori
US-08-471-491-4
alignment_scores:
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US-10-048-197-2 x US-08-470-260-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Covacci, Antonello
APPLICANT: Bugnoli, Massimo
APPLICANT: Telford, John
APPLICANT: Macchia, Giovanni
APPLICANT: Macchia, Giovanni
APPLICANT: Rappuoli, Rino
TITLE OF INVENTION: Helicobacter Py
TITLE OF INVENTION: Diagnostics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Align seg 1/1 to: US-08-470-260-4
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Ratio: 1.000
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 4
LENGTH: 5925
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 601-2708
TELEPAX: (510) 655-3542
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 5925 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4, Application US/08471491B Patent No. 6090611
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PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 08/256,848
FILING DATE: 21-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: MCCLUNG, Barbara G.
REGISTRATION NUMBER: 33,113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/08/471,491B CURRENT FILING DATE: 1995-06-06
                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE: CHIRO044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4801 ATCTCATTTTTGTGGGTAAAA 4821
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CURRENT APPLICATION DATA:
APPLICATION USATA:
APPLICATION UMBER: US/08/470 or FILING DATE:
CLASSITETION OF THE PROPERTY OF THE PR
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TOPOLOGY: lir
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Gaps: 0
Percent Identity: 100.000
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Quality: 7.00 Ratio: 1.000 Percent Similarity: 100.000

7 Gaps: 0 Percent Identity: 100.000

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alignment_block:
US-10-048-197-2 x US-08-471-491-4
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US-10-048-197-2 x US-08-466-662-4
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; ORGANISM: Hellcobacter pylori
US-08-466-662-4
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Quality:
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Percent Similarity: 100.000
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CURRENT FILING DATE: 1995-06-06
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 4
LENGTH: 5925
                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence 3, Application US/08781802 Patent No. 5969121
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APPLICANT: Bugnoll, Massimo
APPLICANT: Bugnoll, Massimo
APPLICANT: Wacchia, Giovanni
APPLICANT: Macchia, Giovanni
APPLICANT: Rappuoll, Rino
TITLE OF INVENTION: Helicobacter Pylori Proteins Useful For Vaccines And
TITLE OF INVENTION: Diagnostics
FILE REFERENCE: CHIR0057
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                      ENERAL INFORMATION:
APPLICANT: AIKEN, Larry
APPLICANT: AIKENS, John
APPLICANT: FONSTEIN, Michael
APPLICANT: VONSTEIN, Veronika
APPLICANT: VONSTEIN, David
APPLICANT: DEMIRJIAN, David
APPLICANT: CASADABAN, Malcolm
TITLE OF INVENTION: Stable Biocatalysts for Ester Hydrolysis
NUMBER OF SEQUENCES: 12
                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS
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                                                                                                               ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff STREET: 300 S. Wacker Drive 32nd Floor CITY: Chicago STATE: Illinois
                                                                          ZIP: 60606
                                                                                              COUNTRY:
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1.000
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seq_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-08-694-078-3
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Ratio: 1.000
Percent Similarity: 100.000
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                                                                                                                                                           Sequence 3, Application US/08694078 Patent No. 6218163 GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                           3635 GAAATTAGCTCCCGCTTCGGA 3615
APPLICANT: ALLEN, Larry
APPLICANT: AIKENS, John
APPLICANT: FONSTEIN, Michael
APPLICANT: VONSTEIN, Veronika
APPLICANT: DEMIRJIAN, David
APPLICANT: CASADABAN, Malcolm
TITLE OF INVENTION: Stable Biocatalysts for Ester Hydrolysis
NUMBER OF SEQUENCES: 8
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APPLICATION NUMBER: US 60/001,995
FILING DATE: 01-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Chao, Mark
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: CDS
LOCATION: 2314..3816
OTHER INFORMATION: /note= "E009 sequence with longest
OTHER INFORMATION: open reading frame; possible other start codons are ATG/me
OTHER INFORMATION: TTG/leu7; GTG/val8; GTG/val15; GTG/val36"
FEATURE:
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TELEPHONE: 312-913-0001
TELEFAX: 312-913-0002
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APPLICATION NUMBER: US 60/019,580
FILING DATE: 12-JUN-1996
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APPLICATION NUMBER: US 08/694,078
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                 51 GluIleSerSerArgPheGly 57
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LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 6263 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 37, REFERENCE/DOCKET NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 07-AUG-1996 CLASSIFICATION: 536
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                                                                                                                                                                                                                                                                                                                                                                                    to reverse of: US-08-781-802-3
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2314..3816
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HER: 95,963-E
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Percent Identity:
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: 0
: 100.000
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CORRESPONDENCE ADDRESS:

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; NAME/KEY:
; LOCATION:
US-08-694-078-3
                                                                                                        seq_documentation_block:
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Quality: 7.00
Ratio: 1.000
Percent Similarity: 100.000
                                                                                                                                      seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-619-554-1
                                                                                                                                                                                                                                                                                               alignment_block:
US-10-048-197-2 x US-08-694-078-3/rev
                                            Sequence 1, Application US/08619554 Patent No. 5821353 GENERAL INFORMATION:
                                                                                                                                                                                                                                                             Align seg 1/1 to reverse of: US-08-694-078-3
                                                                                                                                                                               3635 GAAATTAGCTCCCGCTTCGGA 3615
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TELEFAX: 312-913-0002
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
          APPLICANT:
                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 37,293
REFERENCE/DOCKET NUMBER: 95,
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-213-0001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 60/001,995 FILING DATE: 07-AUG-1995 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 60/009,704 FILING DATE: 10-JAN-1996 PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US 60/019,580
FILING DATE: 12-JUN-1996
                                                                                                                                                                                                                        51 GluIleSerSerArgPheGly 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 12-JUN-1996 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: CDS
LOCATION: 2314..3816
OTHER INFORMATION: /note= "E009 sequence with longest
OTHER INFORMATION: open reading frame; possible other start codons are ATG/met4,
OTHER INFORMATION: TTG/leu7; GTG/val8; GTG/val15; GTG/val36"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
TOPOLOGY: lir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08 FILING DATE: 07-AUG-1996 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 300 S.
CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Chao,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH:
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      DOUGLAS, Cameron M. CHREBET, Gary L.
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2314..3816
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APPLICANT:
                    APPLICANT:
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seq_documentation_block:
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US-10-048-197-2 x US-08-619-554-1
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Quality:
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Ratio: 1.000
Percent Similarity: 100.000
                                                                                     Sequence 56, Application US/08470202 Patent No. 5759808 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: COPPOLA, JOSEPH A
REGISTRATION NUMBER: 38,413
REFERENCE/DOCKET NUMBER: 1910
TELECOMMUNICATION INFORMATION:
TELEPHONE: 732-594-6734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                   APPLICANT:
APPLICANT:
APPLICANT:
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FILING DATE: 01-AUG-19
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                               496 GCCCTCCTTACTGCTCTCCTT 516
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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APPLICANT:
APPLICANT:
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APPLICANT:
APPLICANT:
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ADDRESSEE: JOSEPH A. COPPOLA - MERCK & CO., INC
STREET: 126 EAST LINCOLN AVENUE - P.O. BOX 2000
                                                                                                                                                                                                                                                12 AlaLeuLeuThrAlaLeuLeu 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: KELLY, ROSEMARIE, - PARENT, S.A.
APPLICANT: MARRINAN, Jean, - RAMADAN, N.M.
APPLICANT: MORIN, Nancy, - REGISTER, E.A
APPLICANT: ONISHI, Janet, - SHEI, Gan-Ju
TITLE OF INVENTION: DNA ENCODING 1,3 BETA-D GLUCAN
TITLE OF INVENTION: SYNTHASE SUBUNITS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: 732-594-4720
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SOFTWARE: FastSEC
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Brunn, Albrecht v.
Knapp, Stefan
Hauser, Hans-Peter
                                                   Guertler, Lutz G. Eberle, Josef
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01-AUG-1996
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Gaps: 0
Percent Identity: 100.000
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alignment_block:
US-10-048-197-2 x US-08-470-202-56/rev
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Ratio: 1.000
Percent Similarity: 100.000
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                                                      Sequence 56, Application US/08471770 Patent No. 5770427
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/132,653
FILING DATE: 05-OCT-1993
APPLICATION NUMBER: DE P 42 33 646.5
FILING DATE: 06-OCT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 42 35 718.7
                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: Sir-
TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 9793 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: DE P 42 35 718.7 FILING DATE: 22-OCT-1992 PRIOR APPLICATION DATA: APPLICATION NUMBER: DE P 42 44 541.8 FILING DATE: 30-DEC-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION: TELEPHONE: 202-408-4000
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NAME: Michael J. Blake
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 37,096
REFERENCE/DOCKET NUMBER: 05495-0001-00000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: FILING DATE: 01-JU
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E: Dunner
1300 I Street, N.W.
Guertler, Lutz G
Eberle, Josef
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01-JUN-1993
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Percent Identity: 100.000
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alignment_scores:
Quality:
Ratio:
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US-10-048-197-2 x US-08-471-770-56/rev
seq_documentation_block:
                             seq_name: /cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-468-059-56
                                                                                                                                                                                                                                                                                                                  ; TOPOLOGY: 11;; MOLECULE TYPE: US-08-471-770-56
                                                                                                                                Align seg 1/1 to reverse of: US-08-471-770-56
                                                                                                                                                                                                                 Percent Similarity: 100.000
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                                                              TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 01-JUN-1993
ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: DE P 43 18 186.4
FILING DATE: 01-JUN-1993
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APPLICATION NUMBER: DE P 42 33 646.5
FILING DATE: 06-OCT-1992
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CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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REFERENCE/DOCKET NUMBER: 05495-0001-03000
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ZIP: 20005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Carol P. Einaudi
REGISTRATION NUMBER: 3
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Knapp, Stefan
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Dunner
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22-OCT-1992
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Percent Identity:
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alignment_block:
US-10-048-197-2 x US-08-468-059-56/rev
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Quality:
                                                     Align seg 1/1 to
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                                                                                                                               Quality: 7.00
Ratio: 1.000
Percent Similarity: 100.000
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INFORMATION FOR
11 SerAlaLeuLeuThrAlaLeu 17
                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
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REFERENCE/DOCKET NUMBER: 05,
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Carol P. Einaudi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 42 35 718.7
FILING DATE: 22-CCT-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDLIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P
FILING DATE: 06-0CT-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/132,653
FILING DATE: 05-OCT-1993
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett
ADDRESSEE: Dunner
STREET: 1300 I Street, N.W.
                                                                                                                                                                                                                                                                       STRANDEDNESS:
                                                                                                                                                                                                                                                                                                        LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Retr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/0
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: DE P
FILING DATE: 30-DEC-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 1300 I STATE: Washington
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                                                                                                                                                                                                                                                                                      nucleic acid
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                                                                                                                                                                                                                                                                                                                                                  202-408-4400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
                                              reverse of: US-08-468-059-56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hauser, Hans-Peter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Brunn, Albrecht v.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Knapp, Stefan
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                                                                                                                                                                                                                                       DNA (genomic)
                                                                                                                                                                                                                                                                       single
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01-JUN-1993
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                                                                                                                        Gaps:
Percent Identity:
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                                                                                                                                                        Length:
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: 100.000
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seq_documentation_block:
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US-10-048-197-2 x US-09-109-916-56/rev
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; SEQ ID NO 56
; LENGTH: 9793
; TYPE: DNA
; ORGANISM: Human immunodeficiency virus
US-09-109-916-56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Align seg 1/1 to reverse of: US-09-109-916-56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EARLIER APPLICATION NUMBER: DE P 42 33 646.5
EARLIER FILING DATE: 1992-10-06
EARLIER APPLICATION NUMBER: DE P 42 35 718.7
EARLIER FILING DATE: 1992-10-22
EARLIER APPLICATION NUMBER: DE P 42 44 541.8
EARLIER FILING DATE: 1992-12-30
EARLIER APPLICATION NUMBER: DE P 43 18 186.4
EARLIER FILING DATE: 1993-06-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Quality: 7.00
Ratio: 1.000
Percent Similarity: 100.000
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/477,451
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/08477451
Patent No. 5928865
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                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                 COUNTRY: USA
ZIP: 94608-2916
COMPUTER REALDABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/109,916 CURRENT FILING DATE: 1998-07-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 67
                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Chiron Corporation
STREET: 4560 Horton Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Knapp, Stefan
APPLICANT: Hauser, Hans-Peter
TITLE OF INVENTION: RETROVIRUS FROM HIV GROUP AND ITS USE
FILE REFERENCE: 05495.0001-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Guertler, Lutz
APPLICANT: Eberle, Josef
                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Covacci, TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Brunn, Albrecht V.
                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6097 TCAGCGTTACTTACTGCTCTG 6077
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                                                                                                                                                                                                                                     STATE:
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Ratio:
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                                                                                                                                                                                                                                                  Emeryville
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o. 6277561
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                                                                                                                                                                                                                                                                                                                                           Helicobacter Pylori Cagi Region
                                                                                                                                                                                                                                                                                                                                                                     Antonello
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                                                                                Version #1.30
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ATTORNEY/AGENT INFORMATION:

McClung, Barbara

0335.002

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alignment_scores:
    Quality:
; TOPOLOGY: 1:
; MOLECULE TYPE:
US-08-477-451-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_name: /cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-477-451-5
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Ratio: 1.000
Percent Similarity: 100.000
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Patent No.
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TELEFAX: 510-655-3542
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                       TELEPHONE: 510-601-2708
TELEFAX: 510-655-3542
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 10299 base pairs
                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/477,451
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/ACENT INFORMATION:
NAME: MCClung, Barbara G.
REGISTRATION NUMBER: 33,113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 33,113
REFERENCE/DOCKET NUMBER: 03
TELECOMMUNICATION INFORMATION:
TELEPHONE: 510-601-2708
                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                 REGISTRATION NUMBER: 33,113
REFERENCE/DOCKET NUMBER: 0335.002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 510-601-2708
                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Covacci, Antonello
TITLE OF INVENTION: Helicobacter Pylori Cagi Region
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               90 IleSerPheLeuTrpValLys 96
                                                    STRANDEDNESS:
                                                                          TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
                                      linear
                 DNA (genomic)
                                                      single
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Gaps: 0
Percent Identity: 100.000
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alignment_block:
US-10-048-197-2 x US-08-477-451-5/rev
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Quality:
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US-10-048-197-2 x US-08-477-451-25
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seq_documentation_block:
                                      seq_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-422-869-1
                                                                                                                                                                                                                                                                                                                  alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                           ; MOLECULE TYPE: US-08-477-451-25
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Ratio: 1.000
Percent Similarity: 100.000
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Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: 510-601-270
TELEFAX: 510-655-3542
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6890 ATTTTGAGCTTGATCATTTCG 6910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: McClung, Barbara G. REGISTRATION NUMBER: 33,113 REFERENCE/DOCKET NUMBER: 03: TELECOMMUNICATION INFORMATION: TELEPHONE: 510-601-2708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,451
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: McClung, Barbara G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 94608-2916
ZOMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPACTIBLE
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Covacci, Antonello TITLE OF INVENTION: Helicobac: NUMBER OF SEQUENCES: 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS
                                                                                                                  85 IleLeuSerLeuIleIleSer 91
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TOPOLOGY: 11r
                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
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Ratio:
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                                                                                                                                                                                                                                                                                                                                                                                              DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                     single
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Percent Identity: 100.000
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                                                                                                                                                           to: 19932
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APPLICANT: POLONKY, KENNETH S.

APPLICANT: HORIKAWA, YUKIO

APPLICANT: ODA, NAONISA

APPLICANT: COX, NAONISA

APPLICANT: COX, NAONIS

APPLICANT: SREENAN, SEAMUS

APPLICANT: SREENAN, SEAMUS

APPLICANT: HANIS, CRAIG L.

APPLICANT: HANIS, CRAIG L.

APPLICANT: HANIS, CRAIG L.

APPLICANT: BELL, GRAEME I.

TITLE OF INVENTION: METHODS OF TREATMENT OF TYPE 2 DIABETES

FILE REFERENCE: ARCD:307

CURRENT APPLICATION NUMBER: US/09/422,869

CURRENT APPLICATION NUMBER: 60/134,175

EARLIER APPLICATION NUMBER: 60/134,175

EARLIER FILING DATE: 1999-05-13

NUMBER OF SEQ ID NOS: 30

SOFTWARE: Patentin Ver. 2.0

LENGTH: 49136

TYPE: DNA

ORGANISM: Human

US-09-422-869-1
                                                                                                                                                                                                           alignment_scores:
Quality: 7.00
Ratio: 1.000
Percent Similarity: 100.000
                                                                                                                                        alignment_block:
US-10-048-197-2 x US-09-422-869-1/rev
                                                                                       Align seg 1/1 to reverse of: US-09-422-869-1 from: 1 to: 49136
Sequence 1, Application US/09422869 Patent No. 6235481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                      Length: 7
Gaps: 0
Percent Identity: 100.000
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